

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: May 22, 2002, 15:04:28 ; Search time 55.81 Seconds  
(without alignments)  
772.203 Million cell updates/sec

Title: US-09-596-196-4

Sequence: 1 MMSPOASLFLTNVCIPTG.....PVKIKSVSMKIRMYNYPYK 388

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: A\_Geneseq\_032802.\*

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22: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA2001.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2104	100.0	388	22	Human prothrombina
2	2100	99.8	388	22	Human prothrombina
3	2000	95.1	368	22	Human prothrombina
4	1729	82.2	326	22	Human novel protei
5	1729	82.2	326	22	Human novel protei
6	1625	77.2	306	22	Human prothrombina
7	1299	61.7	237	22	Human prothrombina
8	1265	60.1	240	22	Human prothrombina
9	634	30.1	141	22	Novel human diagno
10	628.5	29.9	138	22	Novel human diagno

RESULT	1	ALIGNMENTS	Novel human diagno
AA82584	standard; Protein; 388 AA.		
XX			
AC	AA82584;		
XX			
DT	02-OCT-2001 (first entry)		
XX			
DE	Human prothrombinase-like polypeptide.		
XX			
KW	Prothrombinase-like polypeptide; human; haemostatic; cardiac;		
KW	nephrotropic; antidiabetic; hepatotropic; antiviral; cytostatic;		
KW	antiartherosclerotic; antitumor; antineoplastic; osteoporosis;		
KW	immunomodulatory; antirheumatic; antithrombotic; antiinflammatory;		
XX	thrombolytic; diagnosis; therapy.		
OS	Homo sapiens.		
XX			
EH	Key	Location/Qualifiers	
FT	Peptide	1..20	
FT	Protein	21..388	
FT		/Label= Signal-peptide	
FT	Domain	/Label= Mature-protein	
FT		/note= "separately claimed in Claim 10"	
FT		/note= "fibrinogen beta/gamma chain"	
FT	Domain	/note= "separately claimed in Claim 10"	
FT		/note= "fibrinogen beta/gamma chain"	
FT		/note= "separately claimed in Claim 10"	
FT	Domain	/note= "fibrinogen beta/gamma chain"	
FT		/note= "separately claimed in Claim 10"	
FT	Domain	324..353	

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FT /note= "fibrinogen beta/gamma chain"  
 FT /note= "separately claimed in Claim 10"  
 PN MO200153456-A2.

XX  
 PD 26-JUL-2001

PF 22-DEC-2000; 2000WO-US35061.  
 XX  
 PR 21-JAN-2000; 2000US-0488725.  
 PR 25-JAN-2000; 2000US-0491404.  
 PR 25-APR-2000; 2000US-0552317.  
 PR 17-JUN-2000; 2000US-0596196.  
 PR 31-AUG-2000; 2000US-0643313.

XX  
 PA (HYSE-) HYSEO INC.  
 PI Haley DA, Boyle BJ, Suk-Yue Ho A, Zhou P, Mize NK, Kuo C;  
 PI Arterburn MC, Tang YN, Liu C, Drmanac R;  
 DR WPI: 2001-483140/52.  
 N-PSDB: AAH26235, AAH26236.

PT Novel prothrombinase-like polypeptides and polynucleotides useful in  
 PT diagnosing and treating e.g. myocardial infarction and diabetes -  
 XX  
 PS Claim 10; Page 126-127; 140pp; English.

XX The present sequence is that of a novel human secreted  
 CC prothrombinase-like polypeptide (PLP). The polypeptide has a  
 CC predicted mol.wt. of 43,000 (unglycosylated) and shows amino acid  
 CC sequence similarity to human prothrombinase Fg12 protein. The  
 CC sequence was predicted from polynucleotides (see AAH26235-36)  
 CC derived from a human ovary cDNA clone. PLP polynucleotides and  
 CC polypeptides, including the mature protein, polypeptides including  
 CC PLP fibrinogen chains, and a soluble splice variant (see AAH82590),  
 CC can be used in the diagnosis, treatment and/or prevention of diseases  
 CC associated with the dysregulation of coagulation pathways, such as  
 CC haemophilia, myocardial infarction, glomerular diseases, diabetes,  
 CC fulminant viral hepatitis and atherosclerosis. They may also be  
 CC beneficial in the treatment of viral infections and some forms of  
 CC cancer. A claimed method of treating a subject in need of enhanced  
 CC PLP activity or expression involves the administration of PLP, a  
 CC PLP agonist or a polynucleotide encoding PLP. A claimed method of  
 CC treating a subject having need to inhibit activity or expression of  
 CC PLP involves the administration of a PLP antagonist, a  
 CC polynucleotide that inhibits expression of a PLP polynucleotide,  
 CC or a polypeptide that competes with the PLP for its ligand. The  
 CC polypeptides can also be used to raise antibodies, as food  
 CC supplements, and to screen for agonists and antagonists.

XX Sequence 388 AA:

Query Match 100.0%; Score 2104; DB 22; Length 388;  
 Best Local Similarity 100.0%; Pred. No. 7.2e-205;  
 Matches 388; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 1 MMSPSQASLFLNLCIFTCGEVVGNCVHSTDSVNVIVEDGSAKAKESKNDTVCKED 60  
 DB 1 mmspsqasllflnclifcgevgncvhsdsvnvivdgsakaksndtvcked 60  
 XX 61 CEESCDVTKTRREKHKMCRNLNLSYSTRSTFKLLRNMMDEQASLDYLSNOVNELM 120  
 DB 61 ceescdvktktrrekhkmcrnlnglsyststfklkllrnmdeqasldylnovnelm 120  
 XX 121 NRVLTLTEVFRKQIDPPHPRVOSHGLDCTDIDKDTISVTKTPSGLYIHPESGSPFE 180  
 DB 121 nrvltltevfrkqidpphprvosghldctdiddkdtisvktktpsglyihpessgspfe 180  
 XX 121 vncdmvrggswtvqkridgltfqrllmcdyldgfgdlgefwlglkkriflyvqknts 240  
 DB 121 vncdmvrggswtvqkridgltfqrllmcdyldgfgdlgefwlglkkriflyvqknts 240

XX 241 FMILYALSEEDTLAASVDNFWLEDETRPFKMLHGRYSGNAGDAFRGLKKEDNONAMPF 300  
 DB 241 fmilyalesedtlayasvdfnwledetrpfkmlhgrysgnagdafrglkkednqnmf 300  
 XX 301 STSDVNDGCRPACLVNNGSVKSCSHLHNKTCGMWNECGLANGLHPSGLKLTATGIOM 360  
 DB 301 stsdvndgcrpactlvngsvskshlnhntcgwmnecglainglhpsgkltatgiow 360  
 XX 361 GTWTKNNSPVKIKSVSMKIRRMVNPYFK 388  
 DB 361 gtwtknnsppvki ksvsmkirmvnpfyk 388

RESULT 2  
 AAY72622  
 ID AAY72622 standard; Protein; 388 AA.  
 AC AAY72622;  
 XX

DT 02-MAY-2001 (first entry)

XX Human: angiotensin; angiotensin; gene therapy; CG144;  
 KW vascular stability; neovascularisation; nutritional supplement; therapy;  
 KW myocardial infarction; proliferative retinopathy; atherosclerosis;  
 KW coronary heart disease; arterial ischemia; bone disorder; cancer;  
 KW abnormal vascular growth; anaemia; chronic inflammation; immune disorder;  
 KW haemopoiesis related disorder; coagulation disorder; leukaemia;  
 KW cytoskeletal; vasotropic; food supplement; nervous system disorder;  
 KW drug screening.

XX Homo sapiens.

XX Key Location/Qualifiers  
 FH Peptide 1..22  
 FT /label= "Signal peptide"  
 FT Protein 23..388  
 FT /note= "Mature angiotensin protein, CG144"  
 FT Domain 193..230  
 FT /note= "Fibrinogen domain"  
 FT Domain 234..247  
 FT /note= "Fibrinogen domain"  
 FT Domain 283..301  
 FT /note= "Fibrinogen domain"  
 FT Domain 307..321  
 FT /note= "Fibrinogen domain"  
 FT Domain 337..366  
 FT /note= "Fibrinogen domain"

XX MO200153456-A2

PD 25-JAN-2001.

XX 17-JUL-2000; 2000WO-US19429.  
 XX 16-JUL-1999; 99US-0354881.

XX (HYSE-) HYSEO INC.  
 PI Ballinger DG, Montgomery JR;  
 DR WPI: 2001-091966/10.  
 N-PSDB: AAD02607.

XX Human angiotensin proteins and DNA encoding sequences useful for  
 PT preventing, treating or ameliorating a medical condition in a mammalian  
 PT subject e.g. arthritis and cancer -  
 XX Claim 10; Page 111-112; 132pp; English.  
 XX The present sequence is human angiotensin protein, CG144.

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CC The present invention relates to human **angiopoietin polypeptides** such  
 CC as CG006, CG007, CG015, CG14 and CG25. The angiopoietin polynucleotides  
 CC are used as hybridisation probes, for chromosome and gene mapping, to  
 CC identify polymorphism and for recombinant protein production.  
 CC Angiopoietin may be useful for modulating vascular stability and  
 CC neovascularisation associated with various pathologies. It is used as a  
 CC nutritional supplement, molecular weight marker and in gene therapy. It  
 CC is also used for preventing, treating or ameliorating angiogenesis  
 CC related disorders such as myocardial infarction, proliferative  
 CC retinopathy, atherosclerosis, coronary heart disease, arterial ischaemia,  
 CC bone disorders (e.g., osteoporosis), abnormal vascular growth, cancer,  
 CC anaemia and chronic inflammatory reactions and autoimmune diseases.  
 CC haematopoiesis related disorders (e.g., myeloid or lymphoid cell  
 CC deficiencies), coagulation disorders, leukaemia and nervous system  
 CC disorders. It is also used in drug screening techniques for screening  
 CC compounds which are able to modulate the expression or activity of  
 CC angiopoietin. The compounds can also be used to treat diseases and  
 CC disorders.

Sequence 388 AA:

Query Match Score 2100; DB 22; Length 388;  
 Best Local Similarity 99.8%; Pred. No. 1.8e-204;  
 Matches 387; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MMSPSQSLFLVNCIFGEGVQNCVHSTDSVYVIVEDGSNAKDESKNDYVCKED 60  
 DB 1 mmspsqslflvncifgegvqncvhsstdsyvniwedgsnadeskndtcked 60  
 QY 61 CEESDVKTKITREEKHEKRNLSIVYSTKTLRNMDQOASLDYLSNOVNEIM 120  
 DB 61 ceesdvkktireekhekrnlisvystsktlrrnmdeqasldylsnvneim 120  
 QY 121 NRVLTLTEVERKQDLPFHPVQSHGLDCTDIKDTIGSVTKPSGLYIIHPEGSSYPE 180  
 DB 121 nrvlltteverkqldpfhprvqshgldctdiktigsvtkpsglyiihpegssype 180  
 QY 121 nrvlltteverkqldpfhprvqshgldctdiktigsvtkpsglyiihpegssype 180  
 QY 161 VMCDMDYRGSGWTYVQKRIIDPQRLWCYLDLGFGLGFWLGLKRIFYVQKNTS 240  
 DB 161 vmcdmdyrgsgwtvqkriddpqrllwcyldlfgfllgfwlglkrlfyvqnkts 240  
 QY 241 FMYLVALESDDTLAYASVNDNFLEDERFEKMHGRYSGNAGDAFRGLKKNONAMPE 300  
 DB 241 fmylvalessddtlayasvndnflwedrfekmhgrysgnagdafrglkknampf 300  
 QY 301 STSDVNDGCRPACLVNGSVKSCSHLNKKTGMFNEGGLANLNGIHHSGLATG10W 360  
 DB 301 stsdvndgcrpactlvngsvskshlnkktgmfnegglanlngihhsqllatg1qW 360  
 QY 361 GTWTKNNSPVKIKSVSMKIRMYNPFK 388  
 DB 361 gtwtknnsppvkiiksvsmtkirmynpfk 388  
 QY 361 gtwtknnsppvkiiksvsmtkirmynpfk 388

RESULT 3

AAB82589 ID AAB82589 standard; Protein; 368 AA.

XX AC AAB82589;

DT 02-OCT-2001 (first entry)

DE Human prothrombinase-like polypeptide (mature protein).

XX Prothrombinase-like polypeptide: human; haemostatic; coagulant;

KW nephrotropic; antidiabetic; hepatotropic; antiviral; cytosolic;

KW antidiabetic; antileukemic; antineurotic; osteoporosis;

KW immunomodulatory; antineurotic; antineurotic; antineurotic;

OS Homo sapiens.

XX Key Location/Qualifiers  
 FH Domain 161..197  
 FT Domain /note="fibrinogen beta/gamma chain"  
 FT Domain 202..214  
 FT Domain /note="fibrinogen beta/gamma chain"  
 FT Domain 251..265  
 FT Domain /note="fibrinogen beta/gamma chain"  
 FT Domain 304..333  
 FT Domain /note="fibrinogen beta/gamma chain"

W0200153456-A2.

PD 26-JUL-2001.

PF 22-DEC-2000; 2000WO-US35061.

PR 21-JAN-2000; 2000US-0488725.

PR 25-JAN-2000; 2000US-0491404.

PR 25-APR-2000; 2000US-0552317.

PR 17-JUN-2000; 2000US-0596196.

PR 31-AUG-2000; 2000US-0643313.

XX (HSE-) HSEQ INC.

XX Haley DA, Boyle BJ, Suk-Yue Ho A, Zhou P, Mize NK, Kuo C;

PI Arterburn MC, Tang YT, Liu C, Drmanac R;

XX WPI: 2001-483140/52.

XX N-PSDB; AAH26235; AAH26236.

XX Claim 10; Page 128-129; 140pp; English.

The present sequence is that of human secreted prothrombinase-like polypeptide (PLP) mature polypeptide, as predicted from polynucleotides (see AAH26235-36) derived from an ovary cDNA clone. PLP polynucleotides and polypeptides, including the mature protein, can be used in the diagnosis, treatment and/or prevention of diseases associated with the dysregulation of coagulation pathways, such as haemophilia, myocardial infarction, glomerular disease, diabetes, fulminant viral hepatitis and atherosclerosis. They may also be beneficial in the treatment of viral infections and some forms of cancer. A claimed method of treating a subject in need of enhanced PLP activity or expression involves the administration of PLP, a PLP agonist or a polynucleotide encoding PLP. A claimed method of treating a subject having need to inhibit activity or expression of PLP involves the administration of a PLP antagonist, a polynucleotide that inhibits expression of a PLP polynucleotide, or a polypeptide that competes with the PLP for its ligand. The polypeptides can also be used to raise antibodies, as food supplements, and to screen for agonists and antagonists.

Sequence 368 AA:

Query Match Score 2000; DB 22; Length 368;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-194;  
 Matches 368; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 EVVQNCVHSTDSVYVIVEDGSNAKDESKNDYVCKEDSCDKTKITREEKHEK 80  
 DB 1 evvqncvhsstdsyvniwedgsnadeskndtckedcdkktireekhefmc 60  
 QY 81 RNLSNIVSYSTRSKKLLRNMDQOASLDYLSNOVNEIMNRVLLTTEVERKQDLPFPH 140  
 DB 61 rnlsvsystrskllrrnmdeqasldylsnvneimnrlltteverkqldpfph 120  
 QY 141 RPVQSHLDCTDIKDTIGSVTKPSGLYIIHPEGSSYPEVWCDMDYRGSGWTYVQKRI 200  
 DB 121 rpvqshldctdiktigsvtkpsglyiihpegssypevwcmdmdyrgsgwtvqkrld 180

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 22, 2002, 15:05:08 ; Search time 22.62 Seconds  
(without alignments)  
418.971 Million cell updates/sec

Title: US-09-596-196-4

Perfect score: 2104

Sequence: 1 MMSPSQASLFLANVICFIG.....PVKIKSVSMKIRMYNPFYK 388

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Optimal number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Issued Patents AA: \*  
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3: /cgnt2\_6/prodata/2/1aa/5a\_COMB.pep.\*  
4: /cgnt2\_6/prodata/2/1aa/5a\_COMB.pep.\*  
5: /cgnt2\_6/prodata/2/1aa/5a\_COMB.pep.\*  
6: /cgnt2\_6/prodata/2/1aa/5a\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	425	20.2	491	2	US-08-933-821-4
2	425	20.2	491	3	US-08-960-507-4
3	425	20.2	491	4	US-09-136-828-4
4	405.5	19.3	480	4	US-08-740-223A-12
5	403.5	19.2	487	4	US-08-740-223A-4
6	402.5	19.1	487	1	US-08-373-579-4
7	402.5	19.1	487	2	US-08-418-595-4
8	402.5	19.1	487	2	US-08-665-926-4
9	402.5	19.1	487	2	US-08-348-492-4
10	402.5	19.1	487	2	US-09-162-437-4
11	400	19.0	483	2	US-08-933-821-2
12	400	19.0	483	3	US-08-960-507-2
13	400	19.0	483	3	US-09-136-828-2
14	399	19.0	483	1	US-08-525-505A-4
15	395.5	18.8	486	4	US-08-740-223A-22
16	395	18.8	486	4	US-08-740-223A-7
17	395	18.8	486	4	US-08-740-223A-26
18	395	18.8	486	4	US-08-740-223A-2
19	395	18.8	486	4	US-09-351-457-2
20	395	18.8	486	4	US-09-351-500-2
21	395	18.8	486	4	US-09-351-108-2
22	394	18.7	485	4	US-08-351-457-5
23	394	18.7	485	4	US-09-351-500-5
24	394	18.7	485	4	US-09-351-108-5
25	393	18.7	491	4	US-08-740-223A-13
26	389	18.5	314	1	US-08-525-505A-2
27	389	18.5	498	1	US-08-373-579-2

28	389	18.5	498	2	US-08-418-595-2	Sequence 2, Appl1
29	389	18.5	498	2	US-08-665-926-2	Sequence 2, Appl1
30	389	18.5	498	2	US-08-348-492-2	Sequence 2, Appl1
31	389	18.5	498	4	US-09-162-437-2	Sequence 2, Appl1
32	387.5	18.4	497	4	US-08-740-223A-14	Sequence 14, Appl1
33	381.5	18.1	480	4	US-08-373-579-6	Sequence 8, Appl1
34	381.5	18.1	496	1	US-08-418-595-6	Sequence 6, Appl1
35	381.5	18.1	496	2	US-08-665-926-6	Sequence 6, Appl1
36	381.5	18.1	496	2	US-09-162-437-6	Sequence 6, Appl1
37	381.5	18.1	496	4	US-08-740-223A-6	Sequence 6, Appl1
38	381.5	18.1	496	4	US-09-351-457-4	Sequence 4, Appl1
39	381.5	18.1	496	4	US-09-561-500-4	Sequence 4, Appl1
40	381.5	18.1	496	4	US-09-561-108-4	Sequence 4, Appl1
41	381.5	18.1	496	4	US-08-740-223A-24	Sequence 24, Appl1
42	381.5	18.1	499	4	US-08-960-507-19	Sequence 19, Appl1
43	381	18.1	346	3	US-08-960-507-19	Sequence 19, Appl1
44	380	18.1	491	1	US-08-206-176-4	Sequence 4, Appl1
45	375.5	17.8				

#### ALIGNMENTS

RESULT 1  
US-08-933-821-4  
Sequence 4, Application US/08933821  
Patent No. 5972328  
GENERAL INFORMATION:  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
TITLE OF INVENTION: Tie Ligands  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESS: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/933,821  
FILING DATE:  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Dregler, Ginger R.  
REGISTRATION NUMBER: 33,055  
REFERENCE/DOCKET NUMBER: P1130  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-3216  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 491 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-933-821-4

Query Match 20.2%, Score 425, DB 2, Length 491;  
Best Local Similarity 26.9%; Pred. No. 1e-35;  
Matches 119; Conservative 64; Mismatch 133; Indels 126; Gaps 14;

QY 44 SNADESKNDYCKECSQDYKITE-EKHFRCRLQNSIYSTSTKRLRNMM 102  
DB 68 TRGDASTIDMTIRMLELKLIVLSROKREIVLQLVVDGNIYNEVLLKRRNNM 127  
QY 103 DE-QQASIDLY-----SNQVEIDMNVLLITTE----- 129

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Db 128 SRVTOPLYMOLLEHRIKRDNSLELSOLENKLINVTTEMLKMATRYRELEVKYASLTDLVN 187  
 Oy 130 -----VFRQ---LDP-----FPHRPVOSHGL----- 148  
 Db 188 NOSVMITLLEBQCLIFRSDTHVSPLVQVPPHAIPIHSQOYTPBLGNETIORDPGYR 247  
 Oy 149 DCTDIDKDTIGSVTKRP-----SGLYIHPEGSSYPREV 181  
 Db 248 DLMPPDLATSPTKSPFKIPPYTFINEGPFKDCQAKKEAGHSVSGIYMIKIPENSNGPMQL 307  
 Oy 182 MCDMDYRGSGWTVIQKRIIDGIIIDFORLWCDYLDGFGDLGFEWGLKRIIFYIVNOKNTSF 241  
 Db 308 WCNESLDPGGWTIVIOKRDGVSYNFRNMENYKKGFGNIDGELWGLGLENYMLSNODN--Y 365  
 Oy 242 MLYVALESEDDTLAVASYDNFWLEDETRFFKMHGIRYSGNAGDAFRGLKREDNQNAMPFS 301  
 Db 366 KLILEEDMSDKKYVAEYSSFRLEPESEFYRLGLTYGNGADSMW-----HNGKQFT 419  
 Oy 302 TSDVDNDCGRACLVNGQSVKCSHLNKTGMWNEGCLANLNGIHHSKLLA---TGI 358  
 Db 420 TLDNRKD-----MYAGNCAHFH-KGGMWYNACAHSLNGLVWYRGHYRSKHODGI 468  
 Oy 359 QMGWTKNNSPVKIKSVSMKIR 380  
 Db 469 FWAEX--RGGSYSLRAVOMMIK 488

RESULT 2  
 US-08-960-507-4  
 : Sequence 4, Application US/08960507  
 : Patent No. 6057435  
 : GENERAL INFORMATION:  
 : APPLICANT: Godowski, Paul J.  
 : APPLICANT: Gurney, Austin L.  
 : TITLE OF INVENTION: The Ligands  
 : NUMBER OF SEQUENCES: 24  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: Genentech, Inc.  
 : STREET: 1 DNA Way  
 : CITY: South San Francisco  
 : STATE: California  
 : COUNTRY: USA  
 : ZIP: 94080  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: Winpatin (Genentech)  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/960.507  
 : FILING DATE:  
 : CLASSIFICATION: 536  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: Dreger, Ginger R.  
 : REGISTRATION NUMBER: 33,055  
 : REFERENCE/DOCKET NUMBER: P1130P1  
 : TELEPHONE: 650/225-3216  
 : TELEFAX: 650/952-9881  
 : INFORMATION FOR SEQ ID NO: 4:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 491 amino acids  
 : TYPE: Amino Acid  
 : TOPOLOGY: Linear  
 : US-08-960-507-4

Query Match 20.2%; Score 425; DB 3; Length 491;  
 Local Similarity 26.9%; Pred. No. 1e-35;  
 Conservative 64; Mismatches 133; Indels 126; Gaps 14;

Db 68 TKGQASTIKDKITRMDELNKLVDLSROKREIDVLQLVVDGNIYNEVKLRKESRMNN 127  
 Oy 103 DE-QQASLDYL-----SNQVNEIMRVLTLTE----- 129  
 Db 128 SRVTOPLYMOLLEHRIKRDNSLELSOLENKLINVTTEMLKMATRYRELEVKYASLTDLVN 187  
 Oy 130 -----VFRQ---LDP-----FPHRPVOSHGL----- 148  
 Db 188 NOSVMITLLEBQCLIFRSDTHVSPLVQVPPHAIPIHSQOYTPBLGNETIORDPGYR 247  
 Oy 149 DCTDIDKDTIGSVTKRP-----SGLYIHPEGSSYPREV 181  
 Db 248 DLMPPDLATSPTKSPFKIPPYTFINEGPFKDCQAKKEAGHSVSGIYMIKIPENSNGPMQL 307  
 Oy 182 MCDMDYRGSGWTVIQKRIIDGIIIDFORLWCDYLDGFGDLGFEWGLKRIIFYIVNOKNTSF 241  
 Db 308 WCNESLDPGGWTIVIOKRDGVSYNFRNMENYKKGFGNIDGELWGLGLENYMLSNODN--Y 365  
 Oy 242 MLYVALESEDDTLAVASYDNFWLEDETRFFKMHGIRYSGNAGDAFRGLKREDNQNAMPFS 301  
 Db 366 KLILEEDMSDKKYVAEYSSFRLEPESEFYRLGLTYGNGADSMW-----HNGKQFT 419  
 Oy 302 TSDVDNDCGRACLVNGQSVKCSHLNKTGMWNEGCLANLNGIHHSKLLA---TGI 358  
 Db 420 TLDNRKD-----MYAGNCAHFH-KGGMWYNACAHSLNGLVWYRGHYRSKHODGI 468  
 Oy 359 QMGWTKNNSPVKIKSVSMKIR 380  
 Db 469 FWAEX--RGGSYSLRAVOMMIK 488

RESULT 3  
 US-09-136-828-4  
 : Sequence 4, Application US/09136828  
 : Patent No. 6350450  
 : GENERAL INFORMATION:  
 : APPLICANT: Godowski, Paul J.  
 : APPLICANT: Gurney, Austin L.  
 : TITLE OF INVENTION: The Ligands  
 : NUMBER OF SEQUENCES: 17  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: Genentech, Inc.  
 : STREET: 1 DNA Way  
 : CITY: South San Francisco  
 : STATE: California  
 : COUNTRY: USA  
 : ZIP: 94080  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: Winpatin (Genentech)  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/09/136.828  
 : FILING DATE:  
 : CLASSIFICATION:  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: Dreger, Ginger R.  
 : REGISTRATION NUMBER: 33,055  
 : REFERENCE/DOCKET NUMBER: P1130R1A  
 : TELEPHONE: 650/225-3216  
 : TELEFAX: 650/952-9881  
 : INFORMATION FOR SEQ ID NO: 4:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 491 amino acids  
 : TYPE: Amino Acid  
 : TOPOLOGY: Linear  
 : US-09-136-828-4

Query Match 20.2%; Score 425; DB 4; Length 491;  
 Best Local Similarity 26.9%; Pred. No. 1e-35;

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 22, 2002, 15:13:50 ; Search time 17.4 Seconds  
(without alignments)  
818.896 Million cell updates/sec

Title: US-09-596-196-9

Perfect score: 2000  
Sequence: 1 EVYQGNCHVHSTDSVYVNV.....PVKIKSVSMKIRRMNYPK 368

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Maximum DB seq length: 0  
Minimum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SWISSProt\_40.\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	413.5	20.7	439	1	Q14314 homo sapien
2	405.5	20.3	432	1	P12804 mus musculu
3	400.5	20.0	481	1	Q18920 bos taurus
4	400.5	20.0	493	1	Q91045 mus musculu
5	400.0	20.0	493	1	Q9uk99 homo sapien
6	398.0	19.9	312	1	Q08830 homo sapien
7	395.5	19.8	468	1	P02876 bos taurus
8	395.5	19.8	498	1	Q15389 homo sapien
9	391.0	19.6	498	1	Q08538 mus musculu
10	381.5	19.1	496	1	Q15123 homo sapien
11	375.5	18.8	491	1	P02675 homo sapien
12	375.5	18.8	375	1	Q07802 bos taurus
13	374.5	18.7	479	1	Q35608 mus musculu
14	373.5	18.7	479	1	P14480 rattus norv
15	371.5	18.6	463	1	Q02020 gallus gall
16	370.0	18.5	477	1	P02678 petromyzon
17	367.5	18.4	453	1	P02679 homo sapien
18	365.0	18.2	444	1	P12799 bos taurus
19	360.0	18.0	432	1	P04115 petromyzon
20	360.0	18.0	509	1	Q9wv16 mus musculu
21	358.0	17.9	503	1	Q9y264 homo sapien
22	352.5	17.6	438	1	P16534 xenopus lae
23	350.5	17.5	282	1	P57756 rattus norv
24	350.5	17.5	282	1	P19477 parastichop
25	348.5	17.4	774	1	P21550 drosophila
26	347.5	16.9	866	1	P02671 homo sapien
27	335.5	16.8	741	1	P14448 gallus gall
28	332.0	16.6	306	1	O70497 mus musculu
29	329.5	16.5	641	1	P23573 petromyzon
30	329.0	16.4	334	1	P07015 mus musculu
31	327.5	16.4	445	1	P02680 rattus norv
32	321.5	16.1	313	1	Q15485 homo sapien
33	321.0	16.1	255	1	P55083 homo sapien

34	313.5	15.7	782	1	F1BA_RAT	P06399 rattus norv
35	310.5	15.5	1808	1	TENX_CHICK	P10039 gallus gall
36	305.5	15.3	335	1	FCN1_RAT	Q9wv18 rattus norv
37	303.5	15.2	326	1	FCN1_HUMAN	O00602 homo sapien
38	302.5	15.1	4289	1	TENX_HUMAN	P22105 homo sapien
39	291.0	14.6	299	1	FCN3_HUMAN	O73636 homo sapien
40	282.5	14.1	1746	1	TENX_PIG	Q29116 sus scrofa
41	271.0	13.6	2201	1	TENX_HUMAN	P24821 homo sapien
42	197.0	9.8	137	1	AGP2_RAT	Q35462 rattus norv
43	109.0	5.5	129	1	MEF4_BOVIN	P55918 bos taurus
44	98.0	4.9	782	1	BICD_DROME	P16568 drosophila
45	97.5	4.9	1432	1	SKI3_YEAST	P17883 saccharomyc

## ALIGNMENTS

RESULT 1  
FGL2\_HUMAN  
ID FGL2\_HUMAN STANDARD: PRT: 439 AA.  
AC Q14314;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Fibrinogen precursor (Fibrinogen-like protein 2) (P149).  
GN Fgl2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Small intestine;  
RX MEDLINE=95369700; PubMed=7642106;  
RA Ruegg C., Pytela R.;  
RT \*Sequence of a human transcript expressed in T-lymphocytes and  
RT encoding a fibrinogen-like protein.";  
RL Gene 160:257-262(1993).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Yuvaraj S., Liu M., Marsden P., Levy G.  
RT \*Cloning and characterization of cDNA for the human counterpart to the  
RT mouse gene Fgl2.  
RL Submitted (NOV-1998) to the EMBL/Genbank/DBJ databases.  
RN [3]  
RP CHARACTERIZATION.  
RX MEDLINE=98309432; PubMed=9647217;  
RA Marzetti S., Blum S., Hartmann R., Gundersen D., Schreyer M.,  
RA Argreaves S., von Flicchner V., Pytela R., Ruegg C.;  
RT \*Characterization of human fibrinogen, a fibrinogen-like protein  
RT secreted by T lymphocytes.";  
RL J. Immunol. 161:138-147(1998).  
RN [4]  
RP FUNCTION: MAY PLAY A ROLE IN PHYSIOLOGIC LYMPHOCYTE FUNCTIONS AT  
RN MUCOSAL SITES.  
CC -1- SUBUNIT: HOMOTETRAMER; DISULFIDE-LINKED.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: CONSTITUTIVELY EXPRESSED IN CYTOTOXIC  
CC T-CELLS.  
CC -1- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC EMBL: Z36531; CAAB5298.1;  
CC DR EMBL: AF104015; AAD10825.1;  
CC DR EMBL: AF104014; AAD10825.1; JOINED.  
CC HSP: P02671.1; LFZD.  
CC MIM: 605351; -.

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DR InterPro: IPR002181; Fibrinogen\_C.  
 DR Pfam: PF00147; fibrinogen\_C.1.  
 DR SMART: SM00186; FBG.1.  
 DR PROSITE: PS00514; FIBRIN-AG\_C\_DOMAIN; 1.  
 KW T-cell; glycoprotein; Signal.  
 FT SIGNAL 1  
 FT CHAIN 1  
 FT DOMAIN 210 435  
 FT DISULFID 213 435  
 FT DISULFID 371 384  
 FT CARBOHYD 25 25  
 FT CARBOHYD 179 179  
 FT CARBOHYD 235 235  
 FT CARBOHYD 263 263  
 FT CARBOHYD 336 336  
 SO SEQUENCE 439 AA; 50228 MW; DF34656288E49E68 CRC64;

Query Match  
 Local Similarity 30.708 Score 413.5; DB 1; Length 439;  
 Matches 119; Conservative 61; Mismatches 147; Indels 67; Gaps 15;

DR 14 SSYVNIVEDSSNAKDESKNDYCKEDCF-----ESCQVYTK 50  
 Db 73 SRIEVEKEVQNKKEIVNSLKKSC-QDCKLQADDNGDPGRNGLLPSTGAPGEVGDNRVR 131  
 QY 51 ITREKHFMCNLONS-IVSYRSTKLLRNM-----MDEQASLDYLSNQVELM 100  
 Db 132 ELSEVVKLSSELKNNAKEIVNLHGREKLTVMNNIENVDSKANLFPVNSLDGKC 191  
 QY 101 NRVLTLTEVFRKQDLPFRPVQSHG--DCTDIKDTIGSVTKPSGLYIIEHGSSTP 158  
 Db 192 SKC-----PSQEQIQSRPVQ-HLHYKDCSDY-----AIGKRSEYKVTDPDNSS 237  
 QY 159 FEWACDMDYRGGWTVQKRIIDGIDPQRLMCDLIDGFDLGFVGLKFIYVQKN 218  
 Db 238 FEYVCDMEWGWTVAQARLDGSTNFTWQDYKAGGNLRREFWGLNDKIHILT--KS 295  
 QY 219 TSFMYALVASEDDTLVASYDNFMLEDETRFFKMLHGRYSGNAGDAFRGLKEDNONAM 278  
 Db 296 KEMLRIDLEFNGVELYALYDOFYVANEFLKRLHVGNYGTGADALR-ENKHYNHDLK 354  
 QY 279 PFTSDVNDGCRPACLVNGOSVKSCHLNKGTGWEVEGLANLNG-IHFSGLKLTATG 337  
 Db 355 FETPPDKNDRYPSG-----NCG-LYSSGWMFPACLSANLNGKYHOKRYGVANG 404  
 QY 338 IOMGTW--TKNNSPYKIKSVSMKIRMYNP-YFK 368  
 Db 405 IFMGTWPGVSAHHPGKYSFKRAKMLIRPKHF 438

RESULT 2  
 FGL2\_MOUSE STANDARD; PRT; 432 AA.  
 ID FGL2\_MOUSE  
 AC 01-OCT-1989 (Rel. 12, Created)  
 DT 01-OCT-1989 (Rel. 12, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Fibrinogen precursor (Fibrinogen-like protein 2) (Prothrombinase)  
 DE (Cytotoxic T-lymphocyte specific protein).  
 GN FGL2 OR FIBLP.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID:10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-cytotoxic T-cell;  
 RX MEDLINE=87175527; PubMed=3550794;  
 RA Koyama T., Hall L.R., Hasegawa S., Salto H.;  
 RT Structure of a cytotoxic T-lymphocyte-specific gene shows a strong  
 RT homology to fibrinogen beta and gamma chains;  
 RT J. Biol. Chem. 267:1609-1613(1992).

[2]  
 RN SEQUENCE FROM N.A., AND CHARACTERIZATION.  
 RP STRAIN-BALB/CJ; TISSUE-peritoneal macrophage;  
 RC MEDLINE=95333285; PubMed=7609073;  
 RA Parr R.L., Fung L., Reneker J., Myers-Mason N., Leibowitz J.L.,  
 RA Levy G.;  
 RT "Association of mouse fibrinogen-like protein with murine hepatitis  
 RT virus-induced prothrombinase activity."  
 RL J. Virol. 69:5033-5038(1995).  
 CC -1- FUNCTION: CONVERTS PROTHROMBIN TO THROMBIN.  
 CC -1- SUBUNIT: HOMOTETRAMER; DISULFIDE-LINKED (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: CONSTITUTIVELY EXPRESSED IN CYTOTOXIC  
 CC T-CELLS.  
 CC -1- INDUCTION: IN MACROPHAGES, DURING INFECTION BY MOUSE HEPATITIS  
 CC VIRUS STRAIN 3 (MHV-3).  
 CC -1- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).

CC EMBL: M16238; AAA37624.1;  
 CC EMBL: M15761; AAA37624.1; JOINED.  
 CC EMBL: S78773; AAB34823.1;  
 CC PIR: A27447; A27447.  
 CC HSSP: P02671; 1FZD.  
 CC MGD: MGI:103266; FGL2.  
 DR InterPro: IPR002181; Fibrinogen\_C.  
 DR Pfam: PF00147; fibrinogen\_C.1.  
 DR SMART: SM00186; FBG.1.  
 DR PROSITE: PS00514; FIBRIN-AG\_C\_DOMAIN; 1.  
 KW T-cell; Cytolysis; Signal.  
 FT SIGNAL 19  
 FT CHAIN 20 432  
 FT DOMAIN 203 428  
 FT DISULFID 206 235  
 FT DISULFID 364 377  
 FT CARBOHYD 24 24  
 FT CARBOHYD 172 172  
 FT CARBOHYD 228 228  
 FT CARBOHYD 256 256  
 FT CARBOHYD 329 329  
 FT CONFLICT 332 332  
 SO SEQUENCE 432 AA; 48951 MW; 2B297F69CBA4A782 CRC64;

Query Match  
 Local Similarity 35.468 Score 405.5; DB 1; Length 432;  
 Best Local Similarity 35.468 Pred. No. 3,7e-25;  
 Matches 110; Conservative 43; Mismatches 115; Indels 43; Gaps 13;

QY 78 LRNMDEQA-----SLDYLSNQVELMNRVLLLTTEVFRKQD-----PFP 119  
 Db 137 LKNADQIOGLQGRLETLHLAVNNIENVYDNKVAANLTVV--NSLDGSKSCPSOEIMQ 194  
 QY 120 HRPVQSHL--DCTDIKDTIGSVTKPSGLYIIEHGSSTPFEWACDMDYRGGWTVQK 177  
 Db 195 SOPVQ-HLHYKDCSD-HYVLG---RRSGATRVDPDHNSSEFYVCDMEWGWTVAQ 249  
 QY 178 RIDGIIDPQRLMCDYLIDGFDLGFVGLKFIYVQKNKTSFMYALVASEDDTLAYA 237  
 Db 250 RLDGSTNFTREWKDYKAGFNLEREFWGLNDKIHILT--KSEMLRIDLDFNGLTLYA 307  
 QY 228 SYDNFMLEDETRFFKMLHGRYSGNAGDAFRGLKEDNONAMPSTSDVNDGCRPACLVN 297  
 Db 308 LYDOFYVANEFLKRLHVGNYGTGADALR-PSRHYNHDLRFTTPDKNDRYPSG----- 362  
 QY 296 GGSVKSCHLNKGTGWEVEGLANLNG-IHFSGLKLTATGSIOMGTWTKNN--SPVKIKS 354

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PF 22-DEC-2000; 2000WO-US35061.

PR 21-JAN-2000; 2000US-0488725.  
PR 25-JAN-2000; 2000US-0491404.  
PR 25-APR-2000; 2000US-0552317.  
PR 17-JUN-2000; 2000US-0596196.  
PR 31-AUG-2000; 2000US-0643313.  
XX  
XX  
XX (HYSE-) HYSEQ INC.  
PI Haley DA, Boyle BJ, Suk-Yue Ho A, Zhou P, Mize NK, Kuo C;  
PI Arterburn MC, Tang YT, Liu C, Drmanac R;  
XX  
XX WPI: 2001-483140/52.  
DR N-PSDB; AAH26235, AAH26236.  
PT Novel prothrombinase-like polypeptides and polynucleotides useful in  
XX diagnosing and treating e.g. myocardial infarction and diabetes -  
XX  
PS Claim 10; Page 128-129; 140pp; English.

CC The present sequence is that of human secreted prothrombinase-like  
CC polypeptide (PLP) mature polypeptide, as predicted from  
CC polynucleotides (see AAH26235-36) derived from an ovary cDNA clone.  
CC PLP polynucleotides and polypeptides, including the mature protein,  
CC can be used in the diagnosis, treatment and/or prevention of diseases  
CC associated with the dysregulation of coagulation pathways, such as  
CC haemophilia, myocardial infarction, glomerular disease, diabetes,  
CC fulminant viral hepatitis and atherosclerosis. They may also be  
CC beneficial in the treatment of viral infections and some forms of  
CC cancer. A claimed method of treating a subject in need of enhanced  
CC PLP activity or expression involves the administration of PLP, a  
CC PLP agonist or a polynucleotide encoding PLP. A claimed method of  
CC treating a subject having need to inhibit activity or expression of  
CC PLP involves the administration of a PLP antagonist, a  
CC polynucleotide that inhibits expression of a PLP polynucleotide,  
CC or a polypeptide that competes with the PLP for its ligand. The  
CC polypeptides can also be used to raise antibodies, as food  
CC supplements, and to screen for agonists and antagonists.  
XX  
XX Sequence 368 AA:

Query Match 100.0%; Score 2000; DB 22; Length 368;  
Best Local Similarity 100.0%; Pred. No. 1.6e-195;  
Matches 368; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EYVQNCVHHSTDDSVNIVEDGSNAKDESKNDTVCKEDCESCDVTKITREKHEHC 60  
Db 1 evvgqncvhhstddsvnlivedgsnakdesksndtvckedceescdvtkitreekhfnc 60  
QY 61 RNLONSIVSYRSTKLLRNMMDEQASLDYLSNOVNELMNVLLLTTFVFRKOLDPFH 120  
Db 61 rnlqnsivsyrcstckllrnmmdesqaaldylsnqvnelmnlvlllttevftrkqldpfph 120  
QY 121 RPYVSHGLDCTDIDKDTISVTKTPESGLYIIHPEGSSYPFEVACDMYRGGGTVIQKRD 180  
Db 121 rpyvshglctdtdidkdtisvctktpesgylilhpegssypfevancdmrygggvtvqkrtd 180  
QY 181 GIIDPQRLMCOYLDGFGDGLGEFWLGLKKIIFYIVNQKNTSEFWLYALSEDDTLAYASYD 240  
Db 181 giidqrlmcoyldgfgdglgefwlglkkiflyivnqkntsefwlyalaseddttlayasyd 240  
QY 241 NFWLEDERFPFKMHLGRYSGNAGDAFRGLKKEDNONAMPFSRSDVDNOCGRACLVNQS 300  
Db 241 nfwledecrfkmhlgrysnaagdafrglkkednqampfssdvdndgcrpactlvnqs 300  
QY 301 VKSCSHLNKGTGMWNEECGLANLNGIIHPSGKLATGIQWGTWTKNNSPVKIKTSVMKIR 360  
Db 301 vkscshlnkgtgmwfnecglanlngihpsgklatgltqwtvctknnspvkiiktsvmktr 360  
QY 361 RMYNPYEK 368  
Db 361 rmynpyk 368

RESULT 2  
AAB82584  
ID AAB82584 standard; Protein; 388 AA.  
XX  
AC AAB82584;  
XX  
XX 02-OCT-2001 (first entry)  
DT  
XX  
XX Human prothrombinase-like polypeptide.  
DE  
XX  
XX Prothrombinase-like polypeptide; human; haemostatic; cardiant;  
KW neptrotropic; antidiabetic; hepatotropic; antiviral; cytostatic;  
KW antiarteriosclerotic; anticancer; vulnerrary; osteoporosis;  
KW immunomodulatory; antirheumatic; antiarthritic; antiinflammatory;  
KW thrombolytic; diagnosis; therapy.  
XX  
XX Homo sapiens.  
OS  
XX  
FH Key Location/Qualifiers  
FH Peptide 1..20  
FT /label- Signal\_peptide  
FT Protein 21..388  
FT /label- Mature\_protein  
FT /note- "separately claimed in Claim 10"  
FT Domain 181..217  
FT /note- "fibrinogen beta/gamma chain"  
FT /note- "separately claimed in Claim 10"  
FT Domain 222..234  
FT /note- "fibrinogen beta/gamma chain"  
FT /note- "separately claimed in Claim 10"  
FT Domain 271..285  
FT /note- "fibrinogen beta/gamma chain"  
FT /note- "separately claimed in Claim 10"  
FT Domain 324..353  
FT /note- "fibrinogen beta/gamma chain"  
FT /note- "separately claimed in Claim 10"  
XX  
XX WO200153456-A2.  
XX  
XX 26-JUL-2001.  
XX  
XX 22-DEC-2000; 2000WO-US35061.  
XX  
XX 21-JAN-2000; 2000US-0488725.  
PR 25-JAN-2000; 2000US-0491404.  
PR 25-APR-2000; 2000US-0552317.  
PR 17-JUN-2000; 2000US-0596196.  
PR 31-AUG-2000; 2000US-0643313.  
XX  
XX (HYSE-) HYSEQ INC.  
PI Haley DA, Boyle BJ, Suk-Yue Ho A, Zhou P, Mize NK, Kuo C;  
PI Arterburn MC, Tang YT, Liu C, Drmanac R;  
XX  
XX WPI: 2001-483140/52.  
DR N-PSDB; AAH26235, AAH26236.  
PT Novel prothrombinase-like polypeptides and polynucleotides useful in  
XX diagnosing and treating e.g. myocardial infarction and diabetes -  
XX  
PS Claim 10; Page 126-127; 140pp; English.

The present sequence is that of a novel human secreted  
CC prothrombinase-like polypeptide (PLP). The polypeptide has a  
CC predicted mol.wt. of 43,000 (unglycosylated) and shows amino acid  
CC sequence similarity to human prothrombinase Fg12 protein. The  
CC sequence was predicted from polynucleotides (see AAH26235-36)  
CC derived from a human ovary cDNA clone. PLP polynucleotides and  
CC polypeptides, including the mature protein, polypeptides including  
CC PLP fibrinogen chains, and a soluble splice variant (see AAB82590),  
CC can be used in the diagnosis, treatment and/or prevention of diseases  
CC associated with the dysregulation of coagulation pathways, such as

CC haemophilia, myocardial infarction, glomerular disease, diabetes,  
CC fulminant viral hepatitis and atherosclerosis. They may also be  
CC beneficial in the treatment of viral infections and some forms of  
CC cancer. A claimed method of treating a subject in need of enhanced  
CC PLP activity or expression involves the administration of PLP, a  
CC PLP agonist or a polynucleotide encoding PLP. A claimed method of  
CC treating a subject having need to inhibit activity or expression of  
CC PLP involves the administration of a PLP antagonist, a  
CC polynucleotide that inhibits expression of a PLP polynucleotide,  
CC or a polypeptide that competes with the PLP for its ligand. The  
CC polypeptides can also be used to raise antibodies, as food  
CC supplements, and to screen for agonists and antagonists.

SO Sequence 388 AA:

Query Match 100.0%; Score 2000; DB 22; Length 388;  
Best Local Similarity 100.0%; Pred. No. 1.7e-195;  
Matches 368; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVVQGNVHHSTSSVYNIYEDGSNAKDESKSDTYCKEDCESCYKRTITREKHFMC 60  
DB 21 EVVQGNVHHSTSSVYNIYEDGSNAKDESKSDTYCKEDCESCYKRTITREKHFMC 80  
QY 61 RNLQNSIVSYTRSTKLLRMMDEQASLDYLSNOVVELMNRVLLTTEVFRKOLDPEPH 120  
DB 81 RNLQNSIVSYTRSTKLLRMMDEQASLDYLSNOVVELMNRVLLTTEVFRKOLDPEPH 140  
QY 121 RPYVSHGLDCTDIKRTIGSVTKTPSGLYIHPGSSYFEVWCDMDYRGSGWTVIQRI 180  
DB 141 RPYVSHGLDCTDIKRTIGSVTKTPSGLYIHPGSSYFEVWCDMDYRGSGWTVIQRI 200  
QY 181 GIIIDPQRIWMDYLDGSGDILGEFNLGKREYIVNOKNTSEFMVYVALESDDPLAVASYD 240  
DB 201 GIIIDPQRIWMDYLDGSGDILGEFNLGKREYIVNOKNTSEFMVYVALESDDPLAVASYD 260  
QY 241 NFWLEDETRFEKMHKLRYSNAGDAFRGLKKEQNONAMPSTSDVDNDGCRPALVQGS 300  
DB 261 NFWLEDETRFEKMHKLRYSNAGDAFRGLKKEQNONAMPSTSDVDNDGCRPALVQGS 320  
QY 301 VKCSHLHNKTKWMEDEGLANTNGIHESGKLATGICMGWTKNNSPVKIKSVSMKIR 360  
DB 321 VKCSHLHNKTKWMEDEGLANTNGIHESGKLATGICMGWTKNNSPVKIKSVSMKIR 380  
QY 361 RMVNPYFK 368  
DB 381 RMVNPYFK 388

RESULT 3  
AAV72622  
ID AAV72622 standard; Protein; 388 AA.  
XX  
AC AAV72622;  
XX  
DT 02-MAY-2001 (first entry)  
XX  
DE Human angiotensin protein, CG144.

XX Human; angiotensin; angiotensin; gene therapy; CG144;  
XX Vascular stability; neovascularisation; nutritional supplement; therapy;  
XX myocardial infarction; proliferative retinopathy; atherosclerosis;  
XX coronary heart disease; arterial ischaemia; bone disorder; cancer;  
XX abnormal vascular growth; anaemia; chronic inflammation; immune disorder;  
XX haematopoiesis related disorder; coagulation disorder; leukaemia;  
XX cytosolic; vasotropic; food supplement; nervous system disorder;  
XX drug screening.

OS Homo sapiens.  
XX  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..22  
FT /Label= Signal\_peptide

FT Protein 23..388  
FT /note= "Mature angiotensin protein, CG144"  
FT Domain 193..230  
FT /note= "Fibrinogen domain"  
FT Domain 234..247  
FT /note= "Fibrinogen domain"  
FT Domain 283..301  
FT /note= "Fibrinogen domain"  
FT Domain 307..321  
FT /note= "Fibrinogen domain"  
FT Domain 337..366  
FT /note= "Fibrinogen domain"

PN 0200005625-12  
PD 25-JAN-2001.

XX 17-JUL-2000; 2000MC-US19429.

XX 16-JUL-1999; 9905-0354881.

XX (HYSE-) HYSEQ INC.

XX Ballinger DG, Montgomery JR;

XX WPI: 2001-091966/10.

XX N-PDB: AAD02607.

PT Human angiotensin proteins and DNA encoding sequences useful for  
PT preventing, treating or ameliorating a medical condition in a mammalian  
PT subject e.g. arthritis and cancer

PS Claim 10; Page 111-112; 132pp; English.

XX The present sequence is human angiotensin protein, CG144.  
XX The present invention relates to human angiotensin polypeptides such  
XX as CG006, CG007, CG015, CG144 and CG250. The angiotensin polynucleotides  
XX are used as hybridisation probes, for chromosome and gene mapping, to  
XX identify polymorphism and for recombinant protein production.  
XX Angiotensin may be useful for modulating vascular stability and  
XX neovascularisation associated with various pathologies. It is used as a  
XX nutritional supplement, molecular weight marker and in gene therapy. It  
XX is also used for preventing, treating or ameliorating angiotensin  
XX related disorders such as myocardial infarction, proliferative  
XX retinopathy, atherosclerosis, coronary heart disease, arterial ischaemia,  
XX bone disorders (e.g., osteoporosis), abnormal vascular growth, cancer,  
XX anaemia and chronic inflammatory reactions (e.g., asthma and arthritis) and immune  
XX disorders (e.g., inflammatory reactions and autoimmune diseases).  
XX haematopoiesis related disorders (e.g., myeloid or lymphoid cell  
XX deficiencies), coagulation disorders, leukaemias and nervous system  
XX disorders. It is also used in drug screening techniques for screening  
XX compounds which are able to modulate the expression or activity of  
XX angiotensin. The compounds can also be used to treat diseases and  
XX disorders.

SO Sequence 388 AA:

Query Match 99.8%; Score 1996; DB 22; Length 388;  
Best Local Similarity 99.7%; Pred. No. 4.3e-195;  
Matches 367; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EVVQGNVHHSTSSVYNIYEDGSNAKDESKSDTYCKEDCESCYKRTITREKHFMC 60  
DB 21 EVVQGNVHHSTSSVYNIYEDGSNAKDESKSDTYCKEDCESCYKRTITREKHFMC 80  
QY 61 RNLQNSIVSYTRSTKLLRMMDEQASLDYLSNOVVELMNRVLLTTEVFRKOLDPEPH 120  
DB 81 RNLQNSIVSYTRSTKLLRMMDEQASLDYLSNOVVELMNRVLLTTEVFRKOLDPEPH 140  
QY 121 RPYVSHGLDCTDIKRTIGSVTKTPSGLYIHPGSSYFEVWCDMDYRGSGWTVIQRI 180  
DB 141 RPYVSHGLDCTDIKRTIGSVTKTPSGLYIHPGSSYFEVWCDMDYRGSGWTVIQRI 200

QY 161 GIIDFQRLMCDYLDGFGDLGFEFWLGLKKIFIVNQKNTSEFMYALASEDDTLAYASYD 240  
CC |||||||  
CC |||||||  
CC 201 gldfgqlwcdyldgfgdlgfefwlglkkifivnqkntsefmyalaseddtlayasyd 260  
QY 241 NFWLEDETRFEFMYHGRYSGNAGDAFRGLKKEEDNONAMPEFSVDVNDNCCPRACLVNGOS 300  
CC |||||||  
CC |||||||  
CC 261 nfwledectrfeffmhlgrysgnagdafrglkkekdnqampfscsdvndnccpracvlvngqs 320  
QY 301 VKSCSHLNKKTGWMEFNECGLANLNGIHHSGLKTLATGIQMGWTFTKNNSPVKIKTSYSMKIR 360  
CC |||||||  
CC |||||||  
CC 321 vkscshlnkktgwmeffnecglanlngihhsyklatgltqwtwtknspvklksysmkir 380  
QY 361 RMYNPFYK 368  
CC |||||||  
CC 381 rmynpfyk 388  
Db  
RESULT 4  
AAB82593 standard; Protein: 306 AA.  
ID AAB82593  
AC AAB82593;  
XX  
XX 02-OCT-2001 (first entry)  
DT  
XX Human prothrombinase-like polypeptide splice variant mature protein.  
DE  
XX Prothrombinase-like polypeptide; human; haemostatic; cardiac;  
KW nephrotropic; antidiabetic; hepatotropic; antiviral; cytostatic;  
KW antiatherosclerotic; antitumor; antitumor; osteoporosis;  
KW immunomodulatory; antitumoral; antitumoral; antitumoral;  
KW chromolytic; diagnosis; therapy.  
XX  
XX Homo sapiens.  
OS  
XX MO200153456-A2.  
PN  
XX 26-JUL-2001.  
PD  
XX 22-DEC-2000; 2000MO-US35061.  
PE  
XX 21-JAN-2000; 2000US-0488725.  
PR 25-JAN-2000; 2000US-0491404.  
PR 25-APR-2000; 2000US-0552317.  
PR 17-JUN-2000; 2000US-0596196.  
PR 31-AUG-2000; 2000US-0643313.  
XX  
XX (HYSE-) HYSEQ INC.  
PA  
XX Haley DA, Boyle BJ, Suk-Yue Ho A, Zhou P, Mize NK, Kuo C;  
PI Arterburn MC, Tang YT, Liu C, Drmanac R;  
PI  
XX WPI: 2001-483140/52.  
DR N-PSDB: AAH26237.  
XX  
XX Novel prothrombinase-like polypeptides and polynucleotides useful in  
PT diagnosing and treating e.g. myocardial infarction and diabetes -  
PT  
XX  
XX Claim 10; Page 135-136; 140pp; English.  
XX  
XX The present sequence is that of the mature portion of a novel  
CC secreted, soluble splice variant (see AAB82590) of novel human  
CC prothrombinase-like polypeptide (PLP). PLP polynucleotides and  
CC polypeptides, including those comprising the mature protein of the  
CC PLP splice variant, can be used in the diagnosis, treatment and/or  
CC prevention of diseases associated with the dysregulation of  
CC coagulation pathways, such as haemophilia, myocardial infarction,  
CC glomerular disease, diabetes, fulminant viral hepatitis and  
CC atherosclerosis. They may also be beneficial in the treatment of  
CC viral infections and some forms of cancer. A claimed method of  
CC treating a subject in need of enhanced PLP activity or expression  
CC involves the administration of PLP, a PLP agonist or a

CC polynucleotide encoding PLP. A claimed method of treating a subject  
CC having need to inhibit activity or expression of PLP involves the  
CC administration of a PLP antagonist, a polynucleotide that inhibits  
CC expression of a PLP polynucleotide, or a polypeptide that competes  
CC with the PLP for its ligand. The polypeptides can also be used to  
CC raise antibodies, as food supplements, and to screen for agonists  
CC and antagonists.  
XX  
XX  
SQ Sequence 306 AA:  
QY 1 EVVQNCVHHSTDDSVYVNIIVEDGSNAKDESKNDYVCKEDCEESCDVKTITREKHFMC 60  
DB 1 evvqncvhhstddsvyniivvedgsnakdeskndyvcckedceescdvktitrekhfmc 60  
QY 61 RNLQNSIVSYSTRSTKLLRNMDQOASLDYLSNOVNEIMNFVLLTTVEFRKQIDPPH 120  
DB 61 rnlqnsivsystrstklrrnmdqoasldylsnovnemnfvllttevfrkqidpph 120  
QY 121 RPVQSHGLDCTDIKDTIGSVTKTPSGLYIHPGSSYPREVWCDMDYRGGWTVIOKRID 180  
DB 121 rpvqshglctdtkdtigsvtktpsglyihpgssyprevwcdmdyrggwvtviokrid 180  
QY 181 GIIDFQRLMCDYLDGFGDLGFEFWLGLKKIFIVNQKNTSEFMYALASEDDTLAYASYD 240  
DB 181 gldfgqlwcdyldgfgdlgfefwlglkkifivnqkntsefmyalaseddtlayasyd 240  
QY 241 NFWLEDETRFEFMYHGRYSGNAGDAFRGLKKEEDNONAMPEFSVDVNDNCCPRACLVNGOS 300  
DB 241 nfwledectrfeffmhlgrysgnagdafrglkkekdnqampfscsdvndnccpracvlvngqs 300  
QY 301 VKSCSHLNKKTGWMEFNECGLANLNGIHHSGLKTLATGIQMGWTFTKNNSPVKIKTSYSMKIR 360  
DB 301 vkscshlnkktgwmeffnecglanlngihhsyklatgltqwtwtknspvklksysmkir 360  
QY 361 RMYNPFYK 368  
DB 361 rmynpfyk 368  
RESULT 5  
AAU14275 standard; Protein: 326 AA.  
ID AAU14275  
AC AAU14275;  
XX  
XX 24-OCT-2001 (first entry)  
DT  
XX Human novel protein #146.  
DE  
XX  
XX Human: novel protein; antianemic; osteopathic; antinflammatory;  
KW immunomodulatory; cytostatic; neuroprotective; vulnary; nocotropic;  
KW antibacterial; antitumor; antitumor; antitumor; antitumor;  
KW chromolytic; immunogen; antibody; gene therapy; neurological disorder;  
KW Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;  
KW tissue regeneration; immune disorder.  
XX  
XX Homo sapiens.  
OS  
XX WO200155437-A2.  
PN  
XX 02-AUG-2001.  
PD  
XX 25-JAN-2001; 2001MO-US02623.  
PR 25-JAN-2000; 2000US-0491404.  
XX  
XX (HYSE-) HYSEQ INC.



The invention relates to polynucleotides encoding novel human proteins or their active domains. The polypeptides, polynucleotides and antibodies raised against the polypeptides are used in a method of treatment of a mammal and prevention of disorders caused by the aberrant protein expression or activity. The polypeptides can be used as molecular weight markers, food supplements, and in antibody production. The polypeptides are used to identify compounds which bind to the polypeptides. Polynucleotides of the invention are used as probes and primers, for sequencing, for chromosome or gene mapping, in the production of recombinant proteins, and in generating anti-sense DNA or RNA and in gene therapy. Polypeptides of the invention can be used to target drugs to a tumour, in assays to determine biological activity, to raise antibodies/elicit an immune response, to determine quantitative protein levels, as tissue markers, and to isolate receptors or ligands. Polypeptides of the invention may also be useful in treating platelet disorders, stem cell disorders, regenerating bone, cartilage, tendon, ligament and/or nerve tissue, wound healing, treating burns, promoting the proliferation, differentiation and survival of stem cells, as a contraceptive, treating osteoporosis and osteoarthritis, anaemia, Alzheimer's, Parkinson's and Huntington's diseases, amyotrophic lateral sclerosis, stroke, immune deficiencies resulting from bacterial, viral or fungal infection or from autoimmunity, cancer, allergy, asthma, graft-versus-host disease, eczema, haemophilia, thrombosis, anti-inflammatory diseases, nervous system disorders, and infection. The present sequence represents a protein of the invention.

```

Oy 1 EYVONCNVCHSHSTDSVVNVIVEDGSSNADDEKSNNTPTVCKEDEECSDVKTITTEDEKIFMC 60
Db 21 evvgncvchshstcdssvnnivcdgssnakdeksnntcvckedecsdvckltteekifmc 80
Oy 61 RNLQNSIVSYSTRSTKTKLLRNMMDEQOASLDYSNQVNELMNRVLLLTTEVFRQOLDFPH 120
Db 81 rnlqnsivsystrsktkllrnmmedeqgsldylsqvnelmrvlllttevfrikqlpfp 140
Oy 121 RPVOSHGLDCTDIKDTIGSVTKTPSGGLYIHPDESSVPEFVCMQDVRGGGWVYQKRI 180
Db 141 rpvoshgldctdikdtkgsvtktpsgglliyhpdeessvpfemcmqdvrgggwvtywkrld 200
Oy 181 GIIDFQRLMCDYLDGFGDGLLEEFMLGLKIFYIVNOKNTSFMLVVALESEDDTLAAVASYD 240
Db 201 giidfrlmcwyldgfggll----- 220
Oy 241 NFMLEDETRFFFMHMLGRVSGNAGDAFRLKEDKNQMAPSTSDVNDGCRPACIVNGOS 300
Db 221 -----gdafrglkredqgnampfstcdvdndgcrpccplvnggs 258
Oy 301 VVSCSHLHNKIGWMEFNECCGLANLNGIHHSFGRLLATGIGQMTWTNKNNSPVKIKSVSMKIR 360
Db 259 vvschllhnkfgwmeegcglanlngihhsfgrllatgigwtwnknnspvkiksvsmkkr 318

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QY	361	RMYPYFK	368
Db	319	rmypnyfk	326

RESULT	6
AAU14511	
ID	AAU14511 standard; Protein; 326 AA.
XX	
AC	AAU14511;
XX	
DT	24-OCT-2001 (first entry)
DE	Human novel protein #382.
XX	
KW	Human; novel protein; Antianaemic; osteopathic; antiinflammatory;
KW	immunomodulatory; cytostatic; neuroprotective; vulnerrary; neotropic;
KW	anticonvulsant; antianthrptic; cerebroprotective; antifungal; antiviral;
KW	antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic;
KW	thrombolytic; immunogen; antibody; gene therapy; neurological disorder;
KW	Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;
XX	tissue regeneration; immune disorder.
OS	Homo sapiens.
XX	
PN	WO200155437-A2.
XX	
PD	02-AUG-2001.
XX	
PE	25-JAN-2001; 2001WO-USO2623.
XX	
PR	25-JAN-2000; 2000US-0491404.
XX	
PPA	(HYSE-) HYSEQ INC.
XX	
PI	Tang YT, Liu C, Drmanac RT;
XX	
WP1	2001-451939/48.
DR	N-PSDB: AAS22816.
XX	
PT	Isolated polypeptides useful for treating anti-inflammatory diseases,
PI	nervous system disorders, and for regenerating bone and cartilage -
XX	
PS	Example 4; Page 848-849; 894pp; English.

Query Match	81.2%;	Score 1625;	DB 22;	Length 326;
Best Local Similarity	83.2%;	Pred. No. 2.7e-157;		
Matches 306;	Conservative 0;	Mismatches 0;	Indels 62;	Gaps 1

```

OY      1 EVVQNCVHSHSTDDSSVNVIVEDGSSNAKDESKSNDTVCKEDCEESCDVKTITREKHEMC 60
        |||||||
DB      21 evvgncvshstddssvnlvedgsnakdesksndtvckedceescdvktltreekhmc 80
        |||||||
OY      61 RMLQNSIVSYTRSTKRLKLNMMDEQOASLDYLSNQVNELMNRYLLTTEVFKQDPPFH 120
        |||||||
DB      81 rmlqnsivsytrstkrllrnmmdqgasldysnqvnelmnrlllttevfkkqldppfh 140
        |||||||
OY      121 RPVQSHGLDCTDIKPTIGSVTKTPSGLYTIHPEGSSYPPEVWCDMDYRGGMVTVIOKRID 180
        |||||||
DB      141 rpvqshgldctdiktptigsvtktpsglytihpessyppevmcdmdyrggwtvliqkrid 200
        |||||||
OY      181 GIIDFQRLMCDYLDGFGDLLGFEFWLGLKKRIFYIVNOKNTSFMLYVLAESDDTLAVASYD 240
        |||||||
DB      201 glidfgrlwcdylldgfgdll----- 220
        |||||||
OY      241 NFWLEDETRFFFKMLHGRYSGNAGDAFRGLKKEDNONAMPFSTSDVNDGCRPACLVNGOS 300
        |||||||
DB      221 -----gdaftrglkkedngnampfstsdvndgcrpactlvngqs 258
        |||||||
OY      301 VKSCSHLHNKTGMWFNEGCLANLNGIHHSGLKLTATGIDMGTWTKNNSPVKIKSVSMKIR 360
        |||||||
DB      259 vkscshlnhktgwfneegclanlngihhtsgkllatgldqwtcknnsppvklksvsmkir 318
        |||||||
OY      361 RMVNPYFK 368
        |||||||
DB      319 rmynpyk 326

RESULT 7
AAB82590
ID      AAB82590 standard; Protein; 326 AA.
XX
AC      AAB82590;
XX
DT      02-OCT-2001 (first entry)
XX
DE      Human prothrombinase-like polypeptide splice variant.
XX
KW      Prothrombinase-like polypeptide; human; haemostatic; cardiac;
KW      nephrotropic; antidiabetic; hepatotropic; antiviral; cytostatic;
KW      antiarteriosclerotic; antilucifer; vulnerrary; osteoporosis;
KW      immunomodulatory; antirheumatic; antitachytic; antinflammatory;
KW      thrombolytic; diagnosis; therapy.
XX
OS      Homo sapiens.
XX
FH      Key
FH      Location/Qualifiers
FT      Peptide
FT      1..20
FT      /label= "Signal peptide"
FT      /note= "separately claimed in Claim 10"
FT      21..326
FT      /label= "Mature protein"
FT      /note= "separately claimed in Claim 10"
FT      181..217
FT      /note= "fibrinogen beta/gamma chain"
FT      262..293
FT      /note= "fibrinogen beta/gamma chain"
FT      82..321
FT      /note= "blood coagulation domain, separately
FT      claimed in Claim 10"
XX
PN      WO200153456-A2.
XX
PD      26-JUL-2001.
XX
PF      22-DEC-2000; 2000WO-US35061.
XX
PR      21-JAN-2000; 2000US-0488725.
PR      25-JAN-2000; 2000US-0491404.
PR      25-APR-2000; 2000US-0552317.
PR      17-JUN-2000; 2000US-0596196.
PR      31-AUG-2000; 2000US-0643313.

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XX      (HYSE-) HYSEO INC.
PA      Haley DA, Boyle BJ, Suk-Yue Ho A, Zhou P, Mize NK, Kuo C;
PI      Arterburn MC, Tang YT, Liu C, Drmanac R;
XX      WPI. 2001-483140/52.
DR      N-PSDB: AAB26237.
XX
PT      Novel prothrombinase-like polypeptides and polynucleotides useful in
PT      diagnosing and treating e.g. myocardial infarction and diabetes -
XX      Claim 10; Page 133; 140pp; English.
PS
XX
CC      The present sequence is that of a secreted, soluble splice variant
CC      of novel human secreted prothrombinase-like polypeptide (PLP, see
CC      also AAB82584). The splice variant has a predicted mol.wt. of
CC      37,000 (unglycosylated) and shows amino acid sequence similarity to
CC      human prothrombinase Fg12 protein. The sequence was predicted from
CC      a polynucleotide (see AAB26237) derived from a human ovary cDNA
CC      clone. PLP polynucleotides and polypeptides, including those
CC      comprising the mature protein, signal peptide or blood coagulation
CC      domain of the splice variant, can be used in the diagnosis,
CC      treatment and/or prevention of diseases associated with the
CC      dysregulation of coagulation pathways, such as haemophilia,
CC      myocardial infarction, glomerular disease, diabetes, fulminant viral
CC      hepatitis and atherosclerosis. They may also be beneficial in the
CC      treatment of viral infections and some forms of cancer. A claimed
CC      method of treating a subject in need of enhanced PLP activity or
CC      expression involves the administration of PLP, a PLP agonist or a
CC      polynucleotide encoding PLP. A claimed method of treating a subject
CC      having need to inhibit activity or expression of PLP involves the
CC      administration of a PLP antagonist, a polynucleotide that inhibits
CC      expression of a PLP polynucleotide, or a polypeptide that competes
CC      with the PLP for its ligand. The polypeptides can also be used to
CC      raise antibodies, as food supplements, and to screen for agonists
CC      and antagonists.
XX
SQ      Sequence 326 AA:

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Query Match      81.2%; Score 1625; DB 22; Length 326;
Best Local Similarity 83.2%; Pred. No. 2,7e-157;
Matches 306; Conservative 0; Mismatches 0; Indels 62; Gaps 1;

OY      1 EVVQNCVHSHSTDDSSVNVIVEDGSSNAKDESKSNDTVCKEDCEESCDVKTITREKHEMC 60
        |||||||
DB      21 evvgncvshstddssvnlvedgsnakdesksndtvckedceescdvktltreekhmc 80
        |||||||
OY      61 RMLQNSIVSYTRSTKRLKLNMMDEQOASLDYLSNQVNELMNRYLLTTEVFKQDPPFH 120
        |||||||
DB      81 rmlqnsivsytrstkrllrnmmdqgasldysnqvnelmnrlllttevfkkqldppfh 140
        |||||||
OY      121 RPVQSHGLDCTDIKPTIGSVTKTPSGLYTIHPEGSSYPPEVWCDMDYRGGMVTVIOKRID 180
        |||||||
DB      141 rpvqshgldctdiktptigsvtktpsglytihpessyppevmcdmdyrggwtvliqkrid 200
        |||||||
OY      181 GIIDFQRLMCDYLDGFGDLLGFEFWLGLKKRIFYIVNOKNTSFMLYVLAESDDTLAVASYD 240
        |||||||
DB      201 glidfgrlwcdylldgfgdll----- 220
        |||||||
OY      241 NFWLEDETRFFFKMLHGRYSGNAGDAFRGLKKEDNONAMPFSTSDVNDGCRPACLVNGOS 300
        |||||||
DB      221 -----gdaftrglkkedngnampfstsdvndgcrpactlvngqs 258
        |||||||
OY      301 VKSCSHLHNKTGMWFNEGCLANLNGIHHSGLKLTATGIDMGTWTKNNSPVKIKSVSMKIR 360
        |||||||
DB      259 vkscshlnhktgwfneegclanlngihhtsgkllatgldqwtcknnsppvklksvsmkir 318
        |||||||
OY      361 RMVNPYFK 368
        |||||||
DB      319 rmynpyk 326

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RESULT 8  
 AAB82582 standard; Protein; 237 AA.  
 ID AAB82582  
 AC AAB82582;  
 XX 02-OCT-2001 (first entry)  
 DE Human prothrombinase-like polypeptide C-terminal region.  
 XX Prothrombinase-like polypeptide; human; haemostatic; cardiant;  
 KW nephrotropic; antidiabetic; hepatotropic; antiviral; cystostatic;  
 KM antiarteriosclerotic; anticulcer; vulnery; osteoporosis;  
 KM immunomodulatory; antirheumatic; antiarthritic; antiinflammatory;  
 KM thrombolytic; diagnosis; therapy.  
 XX Homo sapiens.  
 OS  
 XX Key Location/Qualifiers  
 FH Misc-difference 236  
 FT Misc-difference 237 /note= "encoded by TTT"  
 FT Misc-difference 237 /note= "encoded by AAA"  
 XX MO200153456-A2.  
 XX 26-JUL-2001.  
 PD 22-DEC-2000; 2000MO-US35061.  
 XX 21-JAN-2000; 2000US-0488725.  
 PR 25-APR-2000; 2000US-0491404.  
 PR 25-APR-2000; 2000US-0552317.  
 PR 17-JUN-2000; 2000US-0596196.  
 PR 31-AUG-2000; 2000US-0643313.  
 XX (HYSE-) HYSEQ INC.  
 PA Haley DA, Boyle BJ, Suk-Yue Ho A, Zhou P, Mize NK, Kuo C;  
 PI Arterburn MC, Tang YT, Liu C, Drmanac R;  
 PI WPI: 2001-483140/52.  
 DR N-PSDB: AAB26233.  
 DR Novel prothrombinase-like polypeptides and polynucleotides useful in  
 PT diagnosing and treating e.g. myocardial infarction and diabetes -  
 XX Example 2: Page 108; 140pp; English.  
 XX The present sequence is that of the predicted protein translation  
 CC product of a nucleic acid (see AAB26233) of the invention. It was  
 CC deduced using software that selects a polypeptide based on a  
 CC comparison of translated novel polynucleotides to known polypeptides.  
 CC The sequence shows 38.462% identity to human fibrinogen-like  
 CC protein, and corresponds to the C-terminal portion of a novel  
 CC prothrombinase-like polypeptide (PLP, see AAB82583). PLPs can be  
 CC in the diagnosis, treatment and/or prevention of diseases  
 CC associated with the dysregulation of coagulation pathways, such as  
 CC haemophilia, myocardial infarction, glomerular disease, diabetes,  
 CC fulminant viral hepatitis and atherosclerosis. They may also be  
 CC beneficial in the treatment of viral infections and some forms of  
 CC cancer. A claimed method of treating a subject in need of enhanced  
 CC PLP activity or expression involves the administration of PLP, a  
 CC PLP agonist or a polynucleotide encoding PLP. A claimed method of  
 CC treating a subject having need to inhibit activity or expression of  
 CC PLP involves the administration of a PLP antagonist, a  
 CC polynucleotide that inhibits expression of a PLP polynucleotide,  
 CC or a polypeptide that competes with the PLP for its ligand.  
 CC Sequence 237 AA;  
 SQ

Query Match 65.0%; Score 1299; DB 22; Length 237;  
 Best Local Similarity 99.6%; Pred. No. 3.5e-124;  
 Matches 234; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 OY 132 DIKPTIGSVTKTPSGGLYIHPGSSSYPEVWCDMDYRGGMVYQKRIDGIIDFQRLMCD 191  
 DB 1 dlkdltgsvtktpsgjlyihpgessypfevncdmndyrggvtwqlkridgllidfgrlwcd 60  
 OY 192 YLDGFGDLGFEFWLGKATFEYIVNOKNSFMLYVALESEDDTLVASYDNFLDERPFF 251  
 DB 61 YLDGFGDLGFEFWLGKATFEYIVNOKNSFMLYVALESEDDTLVASYDNFLDERPFF 120  
 OY 252 KMHLGRYSGNAGDAFRLGKKEEDNONAMFSTSDVNDGCRACVNGQSVKSCSHLNKT 311  
 DB 121 kmhlgrysgnagdafrlgkkekdnqampfstsdvndgcrpactlvngqsvkschlnkt 180  
 OY 312 GWMFNECGLANLNGIHHESGKLATGIOWGTWTKNSFVKIKSVSMKIRMYNPY 366  
 DB 181 gwmfnecglanlngihhsgklatlgtwgtwtknspvklksvsmkirmynpy 235  
 RESULT 9  
 AAB82592  
 ID AAB82592 standard; Protein; 240 AA.  
 AC AAB82592;  
 XX 02-OCT-2001 (first entry)  
 DE Human prothrombinase-like polypeptide splice variant domain.  
 XX Prothrombinase-like polypeptide; human; haemostatic; cardiant;  
 KW nephrotropic; antidiabetic; hepatotropic; antiviral; cystostatic;  
 KM antiarteriosclerotic; anticulcer; vulnery; osteoporosis;  
 KM immunomodulatory; antirheumatic; antiarthritic; antiinflammatory;  
 KM thrombolytic; diagnosis; therapy; blood coagulation.  
 XX Homo sapiens.  
 OS  
 XX MO200153456-A2.  
 PN 26-JUL-2001.  
 PD 22-DEC-2000; 2000MO-US35061.  
 XX 21-JAN-2000; 2000US-0488725.  
 PR 25-APR-2000; 2000US-0491404.  
 PR 25-APR-2000; 2000US-0552317.  
 PR 17-JUN-2000; 2000US-0596196.  
 PR 31-AUG-2000; 2000US-0643313.  
 XX (HYSE-) HYSEQ INC.  
 PA Haley DA, Boyle BJ, Suk-Yue Ho A, Zhou P, Mize NK, Kuo C;  
 PI Arterburn MC, Tang YT, Liu C, Drmanac R;  
 PI WPI: 2001-483140/52.  
 DR N-PSDB: AAB26237.  
 DR Novel prothrombinase-like polypeptides and polynucleotides useful in  
 PT diagnosing and treating e.g. myocardial infarction and diabetes -  
 XX Claim 10; Page 134-135; 140pp; English.  
 XX The present sequence is that of the blood coagulation domain of a  
 CC secreted, soluble splice variant (see AAB82590) of novel human  
 CC prothrombinase-like polypeptide (PLP). PLP polynucleotides and  
 CC polypeptides, including those comprising the present domain of the  
 CC PLP splice variant, can be used in the diagnosis, treatment and/or  
 CC prevention of diseases associated with the dysregulation of  
 CC coagulation pathways, such as haemophilia, myocardial infarction,  
 CC glomerular disease, diabetes, fulminant viral hepatitis and  
 CC atherosclerosis. They may also be beneficial in the treatment of

CC viral infections and some forms of cancer. A claimed method of  
CC treating a subject in need of enhanced PLP activity or expression  
CC involves the administration of PLP, a PLP agonist or a  
CC polynucleotide encoding PLP. A claimed method of treating a subject  
CC having need to inhibit activity or expression of PLP involves the  
CC administration of a PLP antagonist, a polynucleotide that inhibits  
CC expression of a PLP polynucleotide, or a polypeptide that competes  
CC with the PLP for its ligand. The polypeptides can also be used to  
CC raise antibodies, as food supplements, and to screen for agonists  
CC and antagonists.  
CC  
XX

Sequence 240 AA:

Query Match 63.2% Score 1265; DB 22; Length 240;  
Best Local Similarity 79.5%; Pred. No. 1.1e-120;  
Matches 240; Conservative 0; Mismatches 0; Indels 62; Gaps 1;

QY 62 NQNSTVSTRSTKTLRMMDQASLDYLSNOVVELMNRVLLTTEVFRKQLDFPHR 121  
DB 1 nqnsivstrstklrmmdeqasldylsnqvnlmrvllltevfirkqldfphr 60  
QY 122 PQQSHGLDCTDKRTIGSVTKTPSGLYIIRPEGSSYFEVMCDMDYRGGMVYIQKRIG 181  
DB 61 pvgshgldctdkrtigsvtktpsglyiirpegsyfevmcdmdyrggwtvirkridg 120  
QY 182 IIDFORLWCDYLDGFGDLDGERWLGKIKTYLVNOKNTSMFLVLESDDTLAVASYDN 241  
DB 121 iidfgrlwcdyldgfgdl----- 139  
QY 242 FWLEDETRFRKHLGRYSGNAGDAFRGLKKEEDNONAMPSTSDVNDGCRPACLVNGOSV 301  
DB 140 -----gdafgrlkkednqampstsdvdndgcrpactlvngsv 178  
QY 302 KSCSHLHNKGTGMWFNECGLANLNGIHMFSGKLLATGICQGTWKNNSPVKIRSVSMKIR 361  
DB 179 kcschlhnkgtgmwfnecglanlngihfsgkllatgicgwtknnsprkiksvsmkrr 238  
QY 362 MY 363  
DB 239 my 240

RESULT 10

ID ABG22365 standard; Protein; 141 AA.

AC ABG22365;

DT 18-FEB-2002 (first entry)

DE Novel human diagnostic protein #22356.

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
KW food supplement; medical imaging; diagnostic; genetic disorder.

OS Homo sapiens.

PN WO200175067-A2.

PD 11-OCT-2001.

PF 30-MAR-2001; 2001WO-US08631.

PR 31-MAR-2000; 2000US-0540217.

PR 23-AUG-2000; 2000US-0649167.

PA (HYSE-) HYSEQ INC.

PI Drmanac RT, Liu C, Tang YT;

DR WPI; 2001-639362/73.

DR N-PSDB; AAS86552.

XX New isolated polynucleotide and encoded polypeptides, useful in  
XX diagnostics, forensics, gene mapping, identification of mutations  
XX responsible for genetic disorders or other traits and to assess  
XX biodiversity -  
XX

PS Claim 20; SEQ ID No 52724; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and  
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,  
XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
XX and gene mapping, and in recombinant production of (II). The  
XX polynucleotides are also used in diagnostics as expressed sequence tags  
XX for identifying expressed genes. (I) is useful in gene therapy techniques  
XX to restore normal activity of (II) or to treat disease states involving  
XX (II). (II) is useful for generating antibodies against it, detecting or  
XX quantitating a polypeptide in tissue, as molecular weight markers and as  
XX a food supplement. (II) and its binding partners are useful in medical  
XX imaging of sites expressing (II). (I) and (II) are useful for treating  
XX disorders involving aberrant protein expression or biological activity.  
XX The polypeptide and polynucleotide sequences have applications in  
XX diagnostics, forensics, gene mapping, identification of mutations  
XX and to produce other types of data and products dependent on DNA and  
XX amino acid sequences. ABG00010-ABG30377 represent novel human  
XX diagnostic amino acid sequences of the invention.  
XX Note: The sequence data for this patent did not appear in the printed  
XX at ftp.wipo.int/pub/published\_pct\_sequences.

Sequence 141 AA:

Query Match 31.7% Score 634; DB 22; Length 141;  
Best Local Similarity 64.3%; Pred. No. 1.5e-56;  
Matches 119; Conservative 1; Mismatches 3; Indels 62; Gaps 1;

QY 158 PREVMCDMDYRGSGWTVYQKRIDGITDFORLWCDYLDGFGDLDGERWLGKIKTYLVNOK 217  
DB 9 pfevmcdmdyrggwtvirkridgitdfgrlwcdyldgfgdl----- 51  
QY 218 NTSFMLVLESDDTLAVASYDNFWLEDETRFRKHLGRYSGNAGDAFRGLKKEEDNONA 277  
DB 52 -----gdafgrlkkednqampstsdvdndgcrpactlvngsv 66  
QY 278 MPFSTSDVNDGCRPACLVNGOSVKSCHLHNKGTGMWFNECGLANLNGIHMFSGKLLATG 337  
DB 67 mpfstsdvndgcrpactlvngosvkschlnhktgmwfnecglanlngihfsgkllatg 126  
QY 338 IOWGT 342  
DB 127 lqwt 131

RESULT 11

ID ABG22361 standard; Protein; 138 AA.

AC ABG22361;

DT 18-FEB-2002 (first entry)

DE Novel human diagnostic protein #22352.

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
KW food supplement; medical imaging; diagnostic; genetic disorder.

OS Homo sapiens.

PN WO200175067-A2.

PD 11-OCT-2001.

XX



XX Human zapo3 protein; angiopoietin-1; angiopoietin-2; covalently linked;  
 KW moiety; affinity tag; toxin; radionuclide; enzyme; fluorophore; multimer;  
 KW coiled coil domain; carboxyl-terminal fibrinogen-like domain; angiogenic;  
 KW haematopoietic; mitogenic activity; angiogenesis; inhibitor;  
 KW endocrine-vascular cell association; revascularisation; DNA probe;  
 KW neuronal degeneration; anti-zapo3 antibody.  
 OS Homo sapiens.  
 XX  
 FH Key  
 FT Location/Qualifiers  
 FT 1..21  
 FT /label= Secretory\_Signal\_Sequence  
 FT Peptide  
 FT 43..48  
 FT /label= Immunogen  
 FT /note= "For production of antibodies"  
 FT 93..98  
 FT /label= Immunogen  
 FT /note= "For production of antibodies"  
 FT 120..125  
 FT /label= Immunogen  
 FT /note= "For production of antibodies"  
 FT 421..426  
 FT /label= Immunogen  
 FT /note= "For production of antibodies"  
 FT 422..427  
 FT /label= Immunogen  
 FT /note= "For production of antibodies"  
 FT 279..490  
 FT /label= Fibrinogen-like domain  
 FT /note= "Homologous to residues 631-864 of human  
 FT fibrinogen alpha chain"  
 FT 63..253  
 FT /label= Amino-terminal\_coiled\_coil\_domain  
 FT MISC-difference  
 FT 280  
 FT /note= "Conserved cysteine residue"  
 FT MISC-difference  
 FT 309  
 FT /note= "Conserved cysteine residue"  
 FT MISC-difference  
 FT 432  
 FT /note= "Conserved cysteine residue"  
 FT MISC-difference  
 FT 445  
 FT /note= "Conserved cysteine residue"  
 XX  
 PN W09940193-A1.  
 XX  
 PD 12-AUG-1999.  
 XX  
 PF 03-FEB-1999; 99WO-US02303.  
 XX  
 PR 04-FEB-1998; 98US-0018258.  
 XX  
 PA (ZYMO ) ZYMOGENETICS INC.  
 XX  
 PI Holloway JL, Shoemaker KE;  
 XX  
 DR WPI: 1999-508503/42.  
 DR N-PSDB: AAX80866.  
 XX  
 PT Human angiopoietin homologue, ZAPO3 useful for study and regulation  
 PT of angiogenesis  
 XX  
 PS Claim 1; Page 65-67; 78pp; English.  
 XX  
 CC The present sequence is a human zapo3 protein. Zapo3 protein exhibits  
 CC significant amino acid sequence homology to angiopoietin-1 and 2. It is  
 CC covalently linked to a moiety chosen from affinity tags, toxins,  
 CC radionuclides, enzymes and fluorophores. The protein is assembled as a  
 CC multimer and is characterized by an amino-terminal coiled coil domain and  
 CC a carboxyl-terminal fibrinogen-like domain. Zapo3 has angiogenic,  
 CC haematopoietic and mitogenic activity. It is useful in the study and  
 CC regulation of angiogenesis, and for developing inhibitors of  
 CC angiogenesis. It is possibly involved in modulation of endocrine-vascular  
 CC cell association and may be used therapeutically to stimulate the

CC revascularisation of tissue, to promote angiogenesis and prevent neuronal  
 CC degeneration. DNA probes and anti-zapo3 antibodies can be used to detect  
 CC sites of angiogenesis.  
 XX  
 XX Sequence 491 AA;  
 SQ  
 Query Match 21.2%; Score 425; DB 20; Length 491;  
 Best Local Similarity 26.9%; Pred. No. 2.2e-34;  
 Matches 119; Conservative 64; Mismatches 133; Indels 126; Gaps 14;  
 QY 24 SNAKDESKNDIVCKEDCECDVKTITRE-EKHFMCNLONSIVSTRSKILLRNM 82  
 DB 68 tkqgdstckmldrmldlenlkdvlsrqkrelvdqglvvdgndlvnevklrkstrmn 127  
 QY 83 DE-QQASLDYL-----SNQVELMNRVLLTTE----- 109  
 DB 128 srvtqlymqlhnelrktrdnlslsqleklntetelmkmalyrelvkyasldlvn 187  
 QY 110 -----VFRKO---LDP-----FPHRPVOSHGL----- 128  
 DB 188 ngsvmltlleeqclrlfsrqdthvsrpilvqvvyvqhlpnsqglpqllggnelqrpgyr 247  
 QY 129 DCTDIKDRIGSVTKRP-----SGYIITHPESSVPEV 161  
 DB 248 dlmprrdlatcpkspfkilprvtflinegrfkdcgakeaghsvsqlymkpnsnpgmql 307  
 QY 162 MCDMDYRGGMVVIQKRIDGIDFQRLMCDYLDGFGDLGFERMLKIKFYLVNOKNTSF 221  
 DB 308 wvensldpggwewlkrtdgsynffrwnenkykkgynldgdeywlhnlmynsqdn--y 365  
 QY 222 MLYVALSEDDPLAYASDNEFWLEDETRFRKMLHGRYSNAGDARGLKEDNQNMPS 281  
 DB 366 klilelwdskkyayesftrlepsefyrllrltlyggnagdsnmw-----hngkqft 419  
 QY 282 TSDVDNDGCRPACLVNGGQVSKSHLHNKTGMFNPDCGLANGLIHFSCKLLA---TGI 338  
 DB 420 lldrdkd-----nyagncalhf-kgywynaacashnlnyvgryghyrskhdgl 468  
 QY 339 CWGTWTKNNSPVKIKSVSMKIR 360  
 DB 469 fwaey--rgsyslrvavgmik 488  
 RESULT 14  
 AAY05397  
 ID AAY05397 standard; Protein; 491 AA.  
 XX  
 AC AAY05397;  
 XX  
 DT 01-JUL-1999 (first entry)  
 XX  
 DE Human TIE ligand NLS protein sequence.  
 XX  
 KW Human TIE ligand; NLS; NL4; NL5; NL8; Ig homology domain; angiogenesis;  
 KW EGF homology domain; receptor tyrosine kinase; vascular endothelial cell;  
 KW early haematopoietic cell; haemopoiesis; neovascularisation; wound healing;  
 KW endothelial cell; growth inhibitor; apoptosis inducer; tumour cell;  
 KW vasculogenesis; detection; diagnosis; therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W09915653-A2.  
 XX  
 PD 01-APR-1999.  
 XX  
 PF 14-SEP-1998; 98WO-US19093.  
 XX  
 PR 29-OCT-1997; 97US-0960507.  
 PR 19-SEP-1997; 97US-0933821.  
 XX  
 PA (GENENTECH ) GENENTECH INC.  
 XX

PI Botstein D, Ferrara N, Goddard A, Godowski PJ, Gurney AL;  
 PI Hillan K, Roy M, Schwall R, Tumas D;  
 XX WPI; 1999-263480/22.  
 DR N-PSDB; AAX36342.  
 XX  
 PT New isolated TIE ligand homologs for, e.g. developing products for  
 treatment of tumors  
 PS  
 XX Claim 8; Fig 5; 132pp; English.  
 XX  
 CC This sequence is the human tyrosine kinase containing Ig and EGF  
 CC homology domains (TIE) ligand of the invention, designated NL5.  
 CC The TIE receptors are receptor tyrosine kinases which are expressed in  
 CC vascular endothelial cells and early hemopoietic cells. The TIE  
 CC receptors are believed to be actively involved in angiogenesis, and may  
 CC play a role in hemopoiesis as well. The TIE ligand homologs can promote  
 CC the survival and/or growth and/or differentiation of TIE receptor  
 CC expressing cells. They can be used for promoting neovascularisation in  
 CC wound healing and for promoting angiogenic processes, such as for  
 CC inducing collateral vascularisation in an ischemic heart or limb, or for  
 CC promoting bone development and/or maturation and/or growth in a patient  
 CC or muscle growth and development. The TIE ligand homologs and antibodies  
 CC can inhibit the growth of endothelial cells and induce apoptosis of  
 CC cells, particularly tumour cells. They can inhibit vasculogenesis,  
 CC particularly the vascularisation of tumour cells. The antibodies can also  
 CC inhibit vascularisation of a cell in which a gene encoding an NL1, NL5,  
 CC NL8 or NL4 polypeptide is amplified. The products can also be used for  
 CC detection, diagnosis, drug screening and production of transgenic  
 CC animals.  
 CC  
 XX  
 SQ Sequence 491 AA:

Query Match 21.24; Score 425; DB 20; Length 491;  
 Best Local Similarity 26.9%; Pred. No. 2.2e-34;  
 Matches 119; Conservative 64; Mismatches 133; Indels 126; Gaps 14;

QY 24 SNADESKNDYVCKEESCVDYKTKTR-EKHFMCRNQNSIVSTRSTKLLRRMM 82  
 DB 68 tkqgdaetldmrlmldkdvlsrqreldvlgvvdvgnlvekvllkrstrmn 127  
 QY 83 DE-QOASLDYV-----SNOVELMNRVLLTTE----- 109  
 DB 128 srvgqlmqllhelikrdmselsqleklnttemklmatyrelvyaaltldvn 187  
 QY 110 -----VFRKQ---LDP-----PFRPVQSHGL----- 128  
 DB 188 nqsvmlclleegclrfstqthvspplvgvpqhlpnsqytlpgllgigneigrdpypr 247  
 QY 129 DCTPIKRTIGSVTKP-----SGLYIIEGSSYPREV 161  
 DB 248 dlmpplatsptkspfkfiprvflinegpfkdcgqakeaghsvsglymlkpeansgmql 307  
 QY 162 MCDMDYRGGWTYQKRFIDIFORLWCDYLDGFDLLGEFGLKRFIFIVOKNTSF 221  
 DB 308 wceaslpqgyvtvlgkrtidgsvmfifmwkkgfmgldgyvlgleniylnsqdn-y 365  
 QY 222 MLVVALESEDDTLAYASYDNFWLDETRFFKMLGRYSGNAGDAFRGLKEDNONAMPFS 281  
 DB 366 klileedwskkyvaesyfrlepesefyrlrlgtygnaqdsmmw-----hngkqft 419  
 QY 282 TSDVDNOCGRACLVNQSOSVSCSHLNKKTGMWNEGGLANLNIHFSGLLA---TGI 338  
 DB 420 tldtdkd-----myagncahfh-kqgwvwnacahsnlgnvvyrgyhrskhdgdl 468  
 QY 339 QMGWTNKNNSPVKIKSVMKIR 360  
 DB 469 fwaey--rggsyslrvavgmik 488

ID AAB24393 standard; Protein: 491 AA.  
 XX AAB24393;  
 AC  
 XX 07-NOV-2000 (first entry)  
 DT  
 XX  
 DE Human PRO188 protein sequence SEQ ID NO:26.  
 XX  
 KW Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation;  
 KW diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy;  
 KW angiogenic; proliferative; cardiact; cardiovascular; antiatherosclerotic;  
 KW cytoslatic; gene therapy; vaccine.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200032221-A2.  
 XX  
 PD 08-JUN-2000.  
 XX  
 PF 30-NOV-1999; 99WO-US28313.  
 XX  
 PR 01-DEC-1998; 98WO-US25108.  
 PR 16-DEC-1998; 98US-0112850.  
 PR 12-JAN-1999; 99US-0115554.  
 PR 08-MAR-1999; 99WO-US05028.  
 PR 12-MAR-1999; 99US-0123957.  
 PR 28-APR-1999; 99US-0131445.  
 PR 14-MAY-1999; 99US-0134287.  
 PR 02-JUN-1999; 99WO-US12252.  
 PR 23-JUN-1999; 99US-0141037.  
 PR 26-JUL-1999; 99US-0144758.  
 PR 26-JUL-1999; 98US-0145698.  
 PR 01-SEP-1999; 99WO-US20111.  
 PR 08-SEP-1999; 99WO-US20594.  
 PR 13-SEP-1999; 99WO-US20944.  
 PR 15-SEP-1999; 99WO-US21090.  
 PR 15-SEP-1999; 99WO-US21547.  
 PR 05-OCT-1999; 99WO-US23089.  
 PR 29-OCT-1999; 99US-0162506.  
 PR  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Hillan KJ, Goddard A;  
 PI Godowski PJ, Gurney AL, Klein RD, Kuo SS, Paoni NF, Smith V;  
 PI Watanabe CK, Williams PM, Wood WT;  
 XX  
 XX WPI; 2000-412154/35.  
 DR N-PSDB; AAA77529.  
 XX  
 PT Nucleic acids encoding PRO polypeptides useful for preventing,  
 PT diagnosing and treating disorders a cardiovascular, endothelial or  
 PT angiogenic disorders in mammals -  
 PS  
 PS Claim 72; Fig 12; 315pp; English.

The present invention describes nucleic acids encoding PRO polypeptides  
 CC useful for preventing, diagnosing and treating disorders in mammals by  
 CC cardiovascular, endothelial or angiogenic disorder in mammals by  
 CC modulating cell proliferation, angiogenesis and cardiovascularisation,  
 CC and for identifying agonists and antagonists of these processes. The  
 CC nucleic acids and the proteins they encode may be used in the  
 CC prevention, treatment and diagnosis of diseases associated with  
 CC inappropriate PRO expression such as cardiovascular, endothelial or  
 CC angiogenic disorders in mammals (e.g. atherosclerosis, cancers and  
 CC cardiac hypertrophy). For example, the nucleic acids (NAs) and vectors  
 CC containing them and the PRO polypeptide may be used to treat disorders  
 CC associated with decreased PRO expression. AAA77510 to AAA77721 and  
 CC AAB24388 to AAB24435 represent nucleotide and protein sequences used in  
 CC the exemplification of the present invention.  
 CC  
 SQ Sequence 491 AA;

RESULT 15  
 AAB24393





[illegible]

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FT      /note= "fibrinogen beta/gamma chain"
FT      /note= "separately claimed in Claim 10"
PN      WO200153456-A2.
XX      26-JUL-2001.
PD      22-DEC-2000; 2000WO-US35061.
PF      21-JAN-2000; 2000US-0488725.
XX      25-JAN-2000; 2000US-0491404.
PR      15-APR-2000; 2000US-0552317.
PR      17-JUN-2000; 2000US-0596196.
XX      31-AUG-2000; 2000US-0643313.
XX      (HYSE-) HYSEQ INC.
XX      Haley DA, Boyle BJ, Suk-Yue Ho A, Zhou P, Mize NK, Kuo C;
PI      Arterburn MC, Yang YT, Liu C, Drmanac R;
XX      WPI: 2001-483140/52.
DR      N-PSDB; AAH26235, AAH26236.
XX      Novel prothrombinase-like polypeptides and polynucleotides useful in
PT      diagnosing and treating e.g. myocardial infarction and diabetes -
XX      Claim 10; Page 126-127; 140pp; English.
XX      The present sequence is that of a novel human secreted
CC      prothrombinase-like polypeptide (PLP). The polypeptide has a
CC      predicted mol.wt. of 43,000 (unglycosylated) and shows amino acid
CC      sequence similarity to human prothrombinase Fg12 protein. The
CC      sequence was predicted from polynucleotides (see AAH26235-36)
CC      derived from a human ovary cDNA clone. PLP polynucleotides and
CC      polypeptides, including the mature protein, polypeptides including
CC      PLP fibrinogen chains, and a soluble splice variant (see AAH82590).
CC      can be used in the diagnosis, treatment and/or prevention of diseases
CC      associated with the dysregulation of coagulation pathways, such as
CC      haemophilia, myocardial infarction, glomerular disease, diabetes,
CC      fulminant viral hepatitis and atherosclerosis. They may also be
CC      beneficial in the treatment of viral infections and some forms of
CC      cancer. A claimed method of treating a subject in need of enhanced
CC      PLP activity or expression involves the administration of PLP, a
CC      PLP agonist or a polynucleotide encoding PLP. A claimed method of
CC      treating a subject having need to inhibit activity or expression of
CC      PLP involves the administration of a PLP antagonist, a
CC      polynucleotide that inhibits expression of a PLP polynucleotide,
CC      or a polypeptide that competes with the PLP for its ligand. The
CC      polypeptides can also be used to raise antibodies, as food
CC      supplements, and to screen for agonists and antagonists.
XX      Sequence 388 AA;
SQ

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QY      241 FMLYVALESEDDTLAYASYADYNFMLEDETRFFKMHILGRVSGNAGDAFRGLKEDQNPMPF 300
DB      241 fmllyvaleseddtlayasyadynfmlēdetrffkmhilygrvsgnagdēfrylkkēdqnampf 300
QY      301 STSDVNDGCRPACLVNGOSVSKSHLHKTGWFRNEGCLAWLNGIHFRSGKLATGIOW 360
DB      301 stsdvndgcrpactlvngosvskshlnkcgwfrnecglanlngthfsgkllatgiqw 360
QY      361 GMTKKNSPVKIKRSVSMKIRRMYNPYEK 388
DB      361 gmtkknspvkiikrsvsmkrrmynpyfk 388

RESULT 2
AAV72622
ID      AAV72622 standard; Protein: 388 AA.
XX      AAV72622;
AC      02-MAY-2001 (first entry)
XX      Human angiotensin protein, CG144.
DE      Human; angiotensin; angiotensin; gene therapy; CG144;
XX      KW vascular stability; neovascularisation; nutritional supplement; therapy;
KW myocardial infarction; proliferative retinopathy; atherosclerosis;
KW coronary heart disease; arterial ischaemia; bone disorder; cancer;
KW abnormal vascular growth; anaemia; chronic inflammation; immune disorder;
KW haematopoiesis related disorder; coagulation disorder; leukaemia;
KW cytostatic; vasotropic; food supplement; nervous system disorder;
KW drug screening.
XX      Homo sapiens.
OS      Homo sapiens.
XX      FH Key
FT      Peptide
FT      1..22 Location/Qualifiers
FT      /label= "Signal_peptide"
FT      /note= "23..388"
FT      Protein
FT      23..388
FT      /note= "Mature angiotensin protein, CG144"
FT      Domain
FT      193..230
FT      /note= "Fibrinogen domain"
FT      234..247
FT      /note= "Fibrinogen domain"
FT      283..301
FT      /note= "Fibrinogen domain"
FT      Domain
FT      307..321
FT      /note= "Fibrinogen domain"
FT      Domain
FT      337..366
FT      /note= "Fibrinogen domain"
XX      PN
XX      WO200105825-A2.
PD      25-JAN-2001.
XX      17-JUL-2000; 2000WO-US19429.
PF      16-JUL-1999; 99US-0354881.
XX      (HYSE-) HYSEQ INC.
XX      Ballinger DG, Montgomery JR;
PI      WPI: 2001-091966/10.
DR      N-PSDB; AAD02607.
XX      Human angiotensin proteins and DNA encoding sequences useful for
PT      preventing, treating or ameliorating a medical condition in a mammalian
PT      subject e.g. arthritis and cancer -
XX      Claim 10; Page 111-112; 132pp; English.
XX      The present sequence is human angiotensin protein, CG144.
CC

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OY 201 GIIDFORLWCDYLDGFGDLGFEFWLGLKKIETIVNOKNTSEMLVYALSEEDDTLAYASVD 260
    |||||||
DB 181 GIIDGFIWCDYLDGFGDLGFEFWLGLKKIETIVNOKNTSEMLVYALSEEDDTLAYASVD 240
OY 261 NWLDEPFEEFMHIGRYSGNAGDAFRGLKKEDNONAMPEFSDVNDGCRPACLVNGOS 320
    |||||||
DB 241 NWLDEPFEEFMHIGRYSGNAGDAFRGLKKEDNONAMPEFSDVNDGCRPACLVNGOS 300
OY 321 VKSCHLHNKGTGWFNECGLANLNGIHHSFGLATGIDMGWTWKNSPVKIKTSYMKIR 380
    |||||||
DB 301 VKSCHLHNKGTGWFNECGLANLNGIHHSFGLATGIDMGWTWKNSPVKIKTSYMKIR 360
OY 381 RMYNPFK 388
    |||||||
DB 361 RMYNPFK 368

RESULT 4
AAU14275
ID AAU14275 standard; Protein: 326 AA.
XX
AC AAU14275;
XX
DT 24-OCT-2001 (first entry)
XX
DE Human novel protein #146.
XX
KW Human; novel protein; Antianaemic; osteopathic; antiinflammatory;
KW immunomodulatory; cytosarctic; neuroprotective; vulnery; nootropic;
KW anticonvulsant; antiallergic; cerebroprotective; antifungal; antiviral;
KW antibacterial; antiallergic; dermatological; haemostatic; antiaesthetic;
KW thrombolytic; immunogen; antibody; gene therapy; neurological disorder;
KW Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;
KW tissue regeneration; immune disorder.
XX
OS Homo sapiens.
XX
PN WO200155437-A2.
XX
PD 02-AUG-2001.
XX
PE 25-JAN-2001; 2001WO-US02623.
XX
PR 25-JAN-2000; 2000US-0491404.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;
XX
DR WPI: 2001-451939/48.
XX
DR N-PSDB: AAS22580.
XX
PT Isolated polypeptides useful for treating anti-inflammatory diseases,
PT nervous system disorders, and for regenerating bone and cartilage -
XX
PS Example 4; Page 605; 894pp; English.
XX
CC The invention relates to polynucleotides encoding novel human
CC proteins or their active domains. The polypeptides, polynucleotides and
CC antibodies raised against the polypeptides are used in a method of
CC treatment of a mammal and prevention of disorders caused by the aberrant
CC protein expression or activity. The polypeptides can be used as
CC molecular weight markers, food supplements, and in antibody production.
CC The polypeptides are used to identify compounds which bind to the
CC polypeptides. Polynucleotides of the invention are used as probes and
CC primers, for sequencing, for chromosome or gene mapping, in the
CC production of recombinant proteins, and in generating anti-sense DNA or
CC RNA and in gene therapy. Polypeptides of the invention can be used to
CC target drugs to a tumour, in assays to determine biological activity, to
CC raise antibodies/elicits an immune response, to determine quantitative
CC protein levels, as tissue markers, and to isolate receptors or ligands.
CC Polypeptides of the invention may also be useful in treating platelet

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CC disorders, stem cell disorders, regenerating bone, cartilage, tendon,
CC ligament and/or nerve tissue, wound healing, treating burns, promoting
CC the proliferation, differentiation and survival of stem cells, as a
CC contraceptive, treating osteoporosis and osteoarthritis, anaemia,
CC Alzheimer's, Parkinson's and Huntington's diseases, amyotrophic lateral
CC sclerosis, stroke, immune deficiencies resulting from bacterial, viral or
CC fungal infection or from autoimmunity, cancer, allergy, asthma,
CC graft-versus-host disease, eczema, haemophilia, thrombosis,
CC anti-inflammatory diseases, nervous system disorders, and infection.
CC The present sequence represents a protein of the invention.
XX
SQ Sequence 326 AA:

Query Match 82.2%; Score 1729; DB 22; Length 326;
Best Local Similarity 84.0%; Pred. No. 7e-167;
Matches 326; Conservative 0; Mismatches 0; Indels 62; Gaps 1;

OY 1 MNSPQASLLFLNVCIFGTGEVYQGCYHNSDSSVYVIVEDGSNAKDESKNDYCKED 60
    |||||||
DB 1 mmspsqasllflnvcifgtgevgncvhsdssvviivedgsnakdesksndtcked 60
OY 61 CEESCDVKTITREKHEFCRNLONSIVSTRSTKLLRNMDQOASLDYLSNOVNEIM 120
    |||||||
DB 61 ceescdvktitreekhfcrcnloinsivstrstkllrnmdeqasldysnqvneim 120
OY 121 NRYLLTTEVFRKQDPPFRPVQSHGLDCTDIKDTIGSVTRTPSGLYIHHEGSSYPE 180
    |||||||
DB 121 nryllttevfrkqdpfrpvqshglctdtkdtigsvtrtpsglyihhegsypye 180
OY 181 VNCMDMYRGGWTVYQKRIDGIIIDFORLWCDYLDGFGDLGFEFWLGLKKIETIVNOKNTS 240
    |||||||
DB 181 vncmdmyrggwvlyqkrldgiiidgfiwcdyldgfgdlgfefwlglkietivnoknts 220
OY 241 FMLYVYALSEEDDTLAYASYDNFWEDETRFEMHIGRYSGNAGDAFRGLKKEDNONAMPE 300
    |||||||
DB 221 -----gdaftrglkkednqampf 238
OY 301 STSDVDNDGCRPACLVNGOSVKSCHLHNKGTGWFNECGLANLNGIHHSFGLATGIDG 360
    |||||||
DB 239 stsdvndgcrpactlvngosvkschlnkgtwfnecglanlngihhsfglatgigw 298
OY 361 GTWTKNSPVKIKTSYMKIRMYNPFK 388
    |||||||
DB 299 gtwtknspvkiiktsysmkirmynyfk 326

RESULT 5
AAU14511
ID AAU14511 standard; Protein: 326 AA.
XX
AC AAU14511;
XX
DT 24-OCT-2001 (first entry)
XX
DE Human novel protein #382.
XX
KW Human; novel protein; Antianaemic; osteopathic; antiinflammatory;
KW immunomodulatory; cytosarctic; neuroprotective; vulnery; nootropic;
KW anticonvulsant; antiallergic; cerebroprotective; antifungal; antiviral;
KW antibacterial; antiallergic; dermatological; haemostatic; antiaesthetic;
KW thrombolytic; immunogen; antibody; gene therapy; neurological disorder;
KW Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;
KW tissue regeneration; immune disorder.
XX
OS Homo sapiens.
XX
PN WO200155437-A2.
XX
PD 02-AUG-2001.
XX
PE 25-JAN-2001; 2001WO-US02623.
XX

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PR 25-JAN-2000; 2000US-0491404.  
 XX (HYSEQ-) HYSEQ INC.  
 PA Tang YT, Liu C, Drmanac RT;  
 PI WPI: 2001-451939/48.  
 DR N-PSDB: AAS22816.  
 XX Isolated polypeptides useful for treating anti-inflammatory diseases,  
 PT nervous system disorders, and for regenerating bone and cartilage -  
 XX  
 PS Example 4; Page 848-849; 894pp; English.  
 XX  
 CC The invention relates to polynucleotides encoding novel human  
 CC proteins or their active domains. The polypeptides, polynucleotides and  
 CC antibodies raised against the polypeptides are used in a method of  
 CC treatment of a mammal and prevention of disorders caused by the aberrant  
 CC protein expression or activity. The polypeptides can be used as  
 CC molecular weight markers, food supplements, and in antibody production.  
 CC The polypeptides are used to identify compounds which bind to the  
 CC polypeptides. Polynucleotides of the invention are used as probes and  
 CC primers, for sequencing, for chromosome or gene mapping. In the  
 CC production of recombinant proteins, and in generating anti-sense DNA or  
 CC RNA and in gene therapy. Polypeptides of the invention can be used to  
 CC target drugs to a tumour, in assays to determine biological activity, to  
 CC raise antibodies/elicit an immune response, to determine quantitative  
 CC protein levels, as tissue markers, and to isolate receptors or ligands.  
 CC Polypeptides of the invention may also be useful in treating platelet  
 CC disorders, stem cell disorders, regenerating bone, cartilage, tendon,  
 CC ligament and/or nerve tissue, wound healing, treating burns, promoting  
 CC the proliferation, differentiation and survival of stem cells, as a  
 CC contraceptive, treating osteoporosis and osteoarthritis, anaemia,  
 CC Alzheimer's, Parkinson's and Huntington's diseases, amyotrophic lateral  
 CC sclerosis, stroke, immune deficiencies resulting from bacterial, viral or  
 CC fungal infection or from autoimmunity, cancer, allergy, asthma,  
 CC graft-versus-host disease, eczema, haemophilia, thrombosis,  
 CC anti-inflammatory diseases, nervous system disorders, and infection.  
 CC The present sequence represents a protein of the invention.  
 CC  
 XX  
 XX Sequence 326 AA:  
 SQ  
 Query Match 82.2%; Score 1729; DB 22; Length 326;  
 Best Local Similarity 84.0%; Pred. No. 7e-167;  
 Matches 326; Conservative 0; Mismatches 0; Indels 62; Gaps 1;  
 QY 1 MMSPSQASLFLNVCIFIGEVGQNCVHSTDSYVNIIVEDGSNAKDESKSNDTVCKED 60  
 DB 1 mmspsqasllflnvcifigevgncvhsdssvnlivedgsnakdesksndtvcked 60  
 QY 61 CEESCDVYKRTTKEKHPHMCNLSYSTRSKTKLLRNAMDQASLDYLSNOVNLML 120  
 DB 61 ceescdvktkttreekhpmcnlnsystsrsktkllrnmddqasldylsnqvnelm 120  
 QY 121 NRVLTLTEVERKQLDPEPHRPVOSHGLDCTDKTIGSVTKTPSGKLYITPEGSSTYFE 180  
 DB 121 nrvtlltteverfkqldephrpvoshgldctdkitgsvtktpsglyitpegsstypfe 180  
 QY 181 VMCDMDYRGGMWTVIQRIDGIDFQRLMCDYLDGFGDLGEFWLGLKRIEYVNOKMTS 240  
 DB 181 vmcdmdyrggmwvtyiqridgidfqrllmcdyldgfgdlgefmlglkrieyvnokm 240  
 QY 241 FMLYVALESEDDTLAYASYDNFMLEDETRFRKMLHGRISGNAAGAFRLGKEDNONAMP 300  
 DB 241 fmlvaleseddtlayasydnfmlwedetrfrkmlhgrtsgnaagafrlgkednonamp 300  
 QY 221 -----gdaftrllkredqnampf 238  
 DB 221 -----gdaftrllkredqnampf 238  
 QY 301 STSDVDNCGCPACLVNCGSVKCSHLNKTGMWNEECGLANLNGIHHSGLATATGIOW 360  
 DB 301 stsdvndngcpcactlvnngsvkscshlnktgmwneecglanlngihhsqllatqigw 360  
 QY 239 stsdvndngcpcactlvnngsvkscshlnktgmwneecglanlngihhsqllatqigw 298  
 DB 239 stsdvndngcpcactlvnngsvkscshlnktgmwneecglanlngihhsqllatqigw 298  
 QY 361 GTWTKNNSPVKIKSVSMKIRRMYNPFYK 388  
 DB 361 gtwtknnsppvki ksvsmkirmynpfyk 388

DB 299 gtwtknnsppvki ksvsmkirmynpfyk 326  
 RESULT 6  
 ID AAB82590 standard; Protein; 326 AA.  
 AC AAB82590;  
 XX  
 XX 02-OCT-2001 (first entry)  
 XX  
 XX Human prothrombinase-like polypeptide splice variant.  
 DE  
 XX  
 KW Prothrombinase-like polypeptide; human; haemostatic; cardiac;  
 KW nephrotropic; antidiabetic; hepatotropic; antiviral; cytostatic;  
 KW antidiabetic; antitumor; anticancer; vulnery; osteoporosis;  
 KW immunomodulatory; antineumatic; antirheumatic; antiinflammatory;  
 XX thrombolytic; diagnosis; therapy.  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FH Peptide 1..20  
 FT /label= Signal\_peptide  
 FT /note= "separately claimed in Claim 10"  
 FT Protein 21..326  
 FT /label= Mature\_protein  
 FT /note= "separately claimed in Claim 10"  
 FT Domain 181..217  
 FT /note= "fibrinogen beta/gamma chain"  
 FT Domain 262..292  
 FT /note= "fibrinogen beta/gamma chain"  
 FT Domain 82..321  
 FT /note= "blood coagulation domain, separately  
 FT claimed in Claim 10"  
 XX  
 XX WO200153456-A2.  
 XX  
 PD 26-JUL-2001.  
 XX  
 XX 22-DEC-2000; 2000WO-US35061.  
 PF  
 XX  
 XX 21-JAN-2000; 2000US-0488725.  
 PR 25-JAN-2000; 2000US-0491404.  
 PR 25-APR-2000; 2000US-0552317.  
 PR 17-JUN-2000; 2000US-0596196.  
 PR 31-AUG-2000; 2000US-0643313.  
 XX  
 PA (HYSEQ-) HYSEQ INC.  
 XX  
 PI Haley DA, Boyle BJ, Suk-Yue Ho A, Zhou P, Mize NK, Kuo C;  
 PI Atterburn MC, Tang YT, Liu C, Drmanac R;  
 DR WPI: 2001-483140/52.  
 DR N-PSDB: AAB26237.  
 XX  
 PT Novel prothrombinase-like polypeptides and polynucleotides useful in  
 PT diagnosing and treating e.g. myocardial infarction and diabetes -  
 XX  
 PS Claim 10; Page 133; 140pp; English.  
 XX  
 CC The present sequence is that of a secreted, soluble splice variant  
 CC of novel human secreted prothrombinase-like polypeptide (PLP, see  
 CC also AAB82584). The splice variant has a predicted mol. wt. of  
 CC 37,000 (unglycosylated) and shows amino acid sequence similarity to  
 CC human prothrombinase Fg12 protein. The sequence was predicted from  
 CC a polynucleotide (see AAB26237) derived from a human ovary cDNA  
 CC clone. PLP polynucleotides and polypeptides, including those  
 CC comprising the mature protein, signal peptide or blood coagulation  
 CC domain of the splice variant, can be used in the diagnosis,  
 CC treatment and/or prevention of diseases associated with the  
 CC dysregulation of coagulation pathways, such as haemophilia,  
 CC myocardial infarction, glomerular disease, diabetes, fulminant viral

hepatitis and atherosclerosis. They may also be beneficial in the treatment of viral infections and some forms of cancer. A claimed method of treating a subject in need of enhanced PLP activity or expression involves the administration of PLP, a PLP agonist or a polynucleotide encoding PLP. A claimed method of treating a subject having need to inhibit activity or expression of PLP involves the administration of a PLP antagonist, a polynucleotide that inhibits expression of a PLP polynucleotide, or a polypeptide that competes with the PLP for its ligand. The polypeptides can also be used to raise antibodies, as food supplements, and to screen for agonists and antagonists.

SQ Sequence 326 AA;

Query Match	82.28	Score 1729	DB 22	Length 326
Best Local Similarly	84.08	Pred. No. 7e-167		
Matches 326	Conservative	0	Mismatches 0	Indels 62
				Gaps 1

QY	1	MASSQASILEPLANCIFJCGEVOGNCVHNHSTDSVYNIVEDSNADEKSDNDTPCKED	60
Dd	1	mmmspsqasllilnvcilfigevagncvhnstsdsvnlvedgsnadeskndtvcyked	60
QY	61	CEESCDVYTKITIREEKHFHMCNHLONSIVSYRTSTKLLRLMMDEOQA5LDLYLSENOVIELM	120
Dd	61	ceescdvYtkitireekhfmcnrlnqslvsyrtstckllrlmmdeqgsldylanqyelml	120
QY	121	NRVLLITTEVFRKOLDPEPRHAPVOSHGLDCTDKDTGSAVYKTPSGLYITHPEGSSYFEE	180
Dd	121	nrvllittevfrkqldpfhrpvsqbsldctldtcltsgvctktpsgylyilhpegsysyfe	180
QY	181	VMCMQMDRGGGWYIYOKRIRIOSIIDEQGLKMDYLDGFECDLLGFEPLGLKIKFYIVNCKNTS	240
Dd	181	vmcmddyrggwcylvlqkrldqldlfdglwcdyldgfgdl-----	220
QY	241	FMLVVALESEDDTLAVASYDNFWLEDETRFEKMHLAGRYSCNAGDAFRGLKEEDNONAMP	3000
Dd	221	-----gdafrglkkeeonqampf	238
QY	301	STSDVDNDGCRPACLIVNGOSVYKSCSHLHNKTGMWFNCEGLANLNGIHHSFSGKLLATGTOW	3600
Dd	239	stsdvdndgcrpaelvngsvkscshlhnktgwwfnecglanlngihhsfgkllaatgicw	298
QY	361	GTWTCKNNSPVAKIKSVSKIRRMKPYRK	388
Dd	299	gtwcknnsppvklksvsmkirtmypyrfk	326

## RESULT

ID AAB82593 standard; Protein; 306 AA.

AC AAB82593;

DT 02-OCT-2001 (first entry)

Human prothrombinase-like polypeptide splice variant mature protein.

KM Prothrombinase-like polypeptide; human; haemostatic; cardiac;  
KM nephrotropic; antidiabetic; hepatotropic; antiviral; cytostatic;  
KM antiarteriosclerotic; antilicer; vulnerary; osteoporosis;  
KM immunomodulatory; antilithematic; antilarthritic; antiinflammatory;  
KM thrombolytic; diagnosis; therapy.

OS Homo sapiens.

PN W0200153456-A2.

PD 26-JUL-2001.

PF 22-DEC-2000; 2000WO-US35061.

PR 21-JAN-2000; 2000US-0488725.

PR 25-JAN-2000; 2000US-0491404.  
PR 25-APR-2000; 2000US-0552317.  
PR 17-JUN-2000; 2000US-0596196.  
PR 31-AUG-2000; 2000US-0643313.

PA (HYSE-) HYSEQ INC

PI Haley DA, Boyle BJ, Suk-Yue Ho A, Zhou P, Mize NK, Kuo C;  
PI Arterburn MC, Tang YT, Liu C, Drymanac R;

DR WPT; 2001-483140/52.

DR N-PSDB; AAH26237.

PT Novel prothrombinase-like polypeptides and polynucleotides useful in  
PT diagnosing and treating e.g. myocardial infarction and diabetes -  
XX  
PS Claim 10; Page 135-136; 140pp; English.

The present sequence is that of the mature portion of a novel secreted, soluble splice variant (see AAB82590) of novel human prothrombinase-like polypeptide (PLP). PLP polynucleotides and polypeptides, including those comprising the mature protein of the PLP splice variant, can be used in the diagnosis, treatment and/or prevention of diseases associated with the dysregulation of coagulation pathways, such as haemophilia, myocardial infarction, glomerular disease, diabetes, fulminant viral hepatitis and atherosclerosis. They may also be beneficial in the treatment of viral infections and some forms of cancer. A claimed method of treating a subject in need of enhanced PLP activity or expression involves the administration of PLP, a PLP agonist or a polynucleotide encoding PLP. A claimed method of treating a subject having need to inhibit activity or expression of PLP involves the administration of a PLP antagonist, a polynucleotide that inhibits expression of a PLP polynucleotide, or a polypeptide that competes with the PLP for its ligand. The polypeptides can also be used to raise antibodies, as food supplements, and to screen for agonists and antagonists.

SQ	Sequence	306	AA;
----	----------	-----	-----

Query Match	77.28;	Score 1625;	DB 22;	Length 306;
Best Local Similarity	83.28;	Pred. No. 2.3e-156;		
Matches 306; Conservative	0;	Mismatches 0;	Indels 62;	Gaps 1;

QY	21	EVWGNCNCHGHSSTSSVNVIVEDGNSNADENKSNQTYCKEDCEECQDVKTYITTRKEHFMC	80
Db	1	evwgncvchbsstssvniivedgsnadesksntckedceecdykltiireekifmc	60
QY	81	RNLQNSIVSYTRSTRKTLRLNMMDQQAQLDYSLNQVLELNMRYLLLTTFEYFRKQDLPFPH	140
Db	61	rnlqnsivsytrseckllrlnmmdqgsldylsnqvelnmrvllltetvfrkqlpfpn	120
QY	141	RPVOSHGLDCTDIDTQTSVTKTPESGLYIHPBESSYRPEEYMCMDYRGGGWYIQKRID	200
Db	121	rpvshgldctdldtqtsvktktpesgllyihpessyrpeemcmdyrgggwviqkrld	180
QY	201	GIIDFORIMCQYLDGFGGGLGEPFLGLKRIYIYNQKNTSMMLYVALESDDTLATVASYD	260
Db	181	giidqtrlmcyldgfgglgsepfllgkriyynqkntsmmlvalesddtlatvasyd	200
QY	261	NFWLEDETRFFKMHILGRYSNAGDAFRGLKLEKEDNQNMPESTDVDNDGCRPACLVNGQS	320
Db	201	nfwledefrfkmhlgrysnagdafrglklekdnqnmpestdvdndgcrpraclvngqs	238
QY	321	VKSCSHLHNKTGMWFNEEGLANLNGIIHFSGRLATSIQGWTKNNSPVKIKSVSKIR	380
Db	239	vkscshlnhktgmwfneeglanlngihfsgklatiglgwtkwnspvklksvsmkir	298
QY	361	RMYNPYEK 388	
Db	299	rmynpyek 306	

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RESULT      8
AAB82582
ID   AAB82582 standard; Protein; 237 AA.
XX
XX   AAB82582;
XX
XX   02-OCT-2001 (first entry)
XX
XX   Human prothrombinase-like polypeptide C-terminal region.
XX
XX   Prothrombinase-like polypeptide; human; haemostatic; cardiant;
XX   nephrotropic; antidiabetic; hepatotropic; antiviral; cyostatic;
XX   antiarteriosclerotic; antilucer; vulnery; osteoporosis;
XX   immunomodulatory; antirheumatic; antiarthritic; antiinflammatory;
XX   thrombolytic; diagnosis; therapy.
XX
XX   Homo sapiens.
XX
XX   Key
XX   Location/Qualifiers
XX   Key
XX   MISC-difference 236
XX   /note= "encoded by TTT"
XX   MISC-difference 237
XX   /note= "encoded by AAA"
XX
XX   MO200153456-A2.
XX
XX   26-JUL-2001.
XX
XX   22-DEC-2000; 2000MO-US35061.
XX
XX   21-JAN-2000; 2000US-0488725.
XX   25-JAN-2000; 2000US-0491404.
XX   25-APR-2000; 2000US-0552317.
XX   17-JUN-2000; 2000US-0596196.
XX   31-AUG-2000; 2000US-0643313.
XX
XX   (HYSE-) HYSEQ INC.
XX
XX   Haley DA, Boyle BJ, Suk-Yue Ho A, Zhou P, Mize NK, Kuo C;
XX   Arterburn MC, Tang YT, Liu C, Drmanac R;
XX
XX   WPI: 2001-483140/52.
XX   N-PSDB: AAB26233.
XX
XX   Novel prothrombinase-like polypeptides and polynucleotides useful in
XX   diagnosing and treating e.g. myocardial infarction and diabetes -
XX
XX   Example 2; Page 108; 140pp; English.
XX
XX   The present sequence is that of the predicted protein translation
XX   product of a nucleic acid (see AAB26233) of the invention. It was
XX   deduced using software that selects a polypeptide based on a
XX   comparison of translated novel polynucleotides to known polypeptides.
XX   The sequence shows 38.462% identity to human fibrinogen-like
XX   protein, and corresponds to the C-terminal portion of a novel
XX   prothrombinase-like polypeptide (PLP, see AAB2583). PLPs can be
XX   in the diagnosis, treatment and/or prevention of diseases
XX   associated with the dysregulation of coagulation pathways, such as
XX   haemophilia, myocardial infarction, glomerular disease, diabetes,
XX   fulminant viral hepatitis and atherosclerosis. They may also be
XX   beneficial in the treatment of viral infections and some forms of
XX   cancer. A claimed method of treating a subject in need of enhanced
XX   PLP activity or expression involves the administration of PLP, a
XX   PLP agonist or a polynucleotide encoding PLP. A claimed method of
XX   treating a subject having need to inhibit activity or expression of
XX   PLP involves the administration of a PLP antagonist, a
XX   polynucleotide that inhibits expression of a PLP polynucleotide,
XX   or a polypeptide that competes with the PLP for its ligand.
XX
XX   Sequence      237 AA;

```

```

Query Match      61.7%; Score 1299; DB 22; Length 237;
Best Local Similarity 99.6%; Pred. No. 2, 1e-123;
Matches 234; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 152 DIKDTIGSVTKTPSGLYIIMEGSSYPEEYVCMDDYRGCGWTYIQKRIDGIIDFQRLMCD 211
DB 1 dlkdtdigsvktktpsglyilimepgssypfevmcndmdyrgcgwtvqkrldgidfgrlwc 60

QY 212 YLDGFGDLGFEFWLGLKIRFIYVQKNTSFMLYALSEDDTLKASYDNWLEDERFF 271
DB 61 yldgfgdlgfefwlglkiflyvqkntsfmlyalseddtlkasydnwledefff 120

QY 272 KMHGGRSGNAGDAPFRGLKREDNONAMPFSVDVNDGCRACLVNCGSVKCSHLNKT 331
DB 121 kmhlgrysnaagdafrglkrednqampfscsdvndgcrpavlrvqsvkscshlnkt 180

QY 332 GWMFNECGLANLNGIHHSKRLATGIQMGTWTRNNSPVKIKSVSMKIRRMYPY 386
DB 181 gwmfnecglanlngihhtsgklatgiqmgtwtrnnspsvkiksvsmkirmrnp 235

RESULT      9
AAB82592
ID   AAB82592 standard; Protein; 240 AA.
XX
XX   AAB82592;
XX
XX   02-OCT-2001 (first entry)
XX
XX   Human prothrombinase-like polypeptide splice variant domain.
XX
XX   Prothrombinase-like polypeptide; human; haemostatic; cardiant;
XX   nephrotropic; antidiabetic; hepatotropic; antiviral; cyostatic;
XX   antiarteriosclerotic; antilucer; vulnery; osteoporosis;
XX   immunomodulatory; antirheumatic; antiarthritic; antiinflammatory;
XX   thrombolytic; diagnosis; therapy; blood coagulation.
XX
XX   Homo sapiens.
XX
XX   W0200153456-A2.
XX
XX   26-JUL-2001.
XX
XX   22-DEC-2000; 2000MO-US35061.
XX
XX   21-JAN-2000; 2000US-0488725.
XX   25-JAN-2000; 2000US-0491404.
XX   25-APR-2000; 2000US-0552317.
XX   17-JUN-2000; 2000US-0596196.
XX   31-AUG-2000; 2000US-0643313.
XX
XX   (HYSE-) HYSEQ INC.
XX
XX   Haley DA, Boyle BJ, Suk-Yue Ho A, Zhou P, Mize NK, Kuo C;
XX   Arterburn MC, Tang YT, Liu C, Drmanac R;
XX
XX   WPI: 2001-483140/52.
XX   N-PSDB: AAB26237.
XX
XX   Novel prothrombinase-like polypeptides and polynucleotides useful in
XX   diagnosing and treating e.g. myocardial infarction and diabetes -
XX
XX   Claim 10; Page 134-135; 140pp; English.
XX
XX   The present sequence is that of the blood coagulation domain of a
XX   secreted, soluble splice variant (see AAB82590) of novel human
XX   prothrombinase-like polypeptide (PLP). PLP polynucleotides and
XX   polypeptides, including those comprising the present domain of the
XX   PLP splice variant, can be used in the diagnosis, treatment and/or
XX   prevention of diseases associated with the dysregulation of
XX   coagulation pathways, such as haemophilia, myocardial infarction,
XX   glomerular disease, diabetes, fulminant viral hepatitis and
XX   atherosclerosis. They may also be beneficial in the treatment of

```

CC viral infections and some forms of cancer. A claimed method of  
CC treating a subject in need of enhanced PLP activity or expression  
CC involves the administration of PLP, a PLP agonist or a  
CC polynucleotide encoding PLP. A claimed method of treating a subject  
CC having need to inhibit activity or expression of PLP involves the  
CC administration of a PLP antagonist, a polynucleotide that inhibits  
CC expression of a PLP polynucleotide, or a polypeptide that competes  
CC with the PLP for its ligand. The polypeptides can also be used to  
CC raise antibodies, as food supplements, and to screen for agonists  
CC and antagonists.  
CC  
XX  
SQ Sequence 240 AA:  
  
Query Match 60.1%; Score 1265; DB 22; Length 240;  
Best Local Similarity 79.5%; Pred. No. 6.1e-120;  
Matches 240; Conservative 0; Mismatches 0; Indels 62; Gaps 1;  
  
OY 82 NTONSVSTRSTKKLLRNMDEQASIDYLSNOVELMKNRVLLLTTEVFRKOLDPEPR 141  
DB 1 ntgnsvstrstkkllrnmdeqasidylsnqvelmknrvlllttevfrrkldpfpnr 60  
OY 142 PVQSHGLDCTDIKDTIGSVTKTPSGLYITNPGSSVYFEVMCDMDYRGSGWTVTQKRIG 201  
DB 61 pvqshgldctdtkdtigsvtktpsglyitnpgssvfyfvmcdmdyrgsgwtvtqkridg 120  
OY 202 ITDFORLWCMDYLDGFGDLGFEFWLGLKRTFYVNOKNTSFMLYVALESDPTLAVASYDN 261  
DB 121 itdfgrlwcodyldgfgdl----- 139  
OY 262 FWLEDETRFRFKHNLGRYSGNAGDAFRGLKKEEDNONAMPSTSDVDNDGCRPACLVNGOSV 321  
DB 140 -----gdaftrglkkednampstsdvdndgcrpactlvnqgsv 178  
OY 322 KSCSHLHNKKTGMWFNECGLANLNGIHNEGSKLLATGICOMGTWKNNSPVKIKSVSKIRR 381  
DB 179 kscshlnhktgwmfnecglaingihnefsgkllatgicwtgknnspvkiiksvsmkirt 238  
OY 382 MY 383  
DB 239 my 240  
  
RESULT 10  
ABG22365  
ID ABG22365 standard; Protein, 141 AA.  
XX  
AC ABG22365;  
XX  
DT 18-FEB-2002 (first entry)  
XX  
DE Novel human diagnostic protein #22356.  
XX  
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
KW food supplement; medical imaging; diagnostic; genetic disorder.  
XX  
OS Homo sapiens.  
XX  
PN WO200175067-A2.  
XX  
PD 11-OCT-2001.  
XX  
PE 30-MAR-2001; 2001WO-US08631.  
XX  
PR 31-MAR-2000; 2000US-0540217.  
PR 23-AUG-2000; 2000US-0649167.  
XX  
PA (HYSE-) HYSEQ INC.  
XX  
PI Drmanac RT, Liu C, Tang YT;  
XX  
XX WPI; 2001-639362/73.  
DR N-PSDB; AAS86552.

XX  
PT New isolated polynucleotide and encoded polypeptides, useful in  
PT diagnostics, forensics, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
PT biodiversity.  
XX  
PS Claim 20; SEQ ID NO 52724; 103pp; English.  
XX  
CC The invention relates to isolated polynucleotide (I) and  
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,  
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
CC and gene mapping, and in recombinant production of (II). The  
CC polynucleotides are also used in diagnostics as expressed sequence tags  
CC for identifying expressed genes. (I) is useful in gene therapy techniques  
CC to restore normal activity of (II) or to treat disease states involving  
CC (II). (II) is useful for generating antibodies against it, detecting or  
CC quantitating a polypeptide in tissue, as molecular weight markers and as  
CC a food supplement. (II) and its binding partners are useful in medical  
CC imaging of sites expressing (II). (I) and (II) are useful for treating  
CC disorders involving aberrant protein expression or biological activity.  
CC The polypeptide and polynucleotide sequences have applications in  
CC diagnostics, forensics, gene mapping, identification of mutations  
CC responsible for genetic disorders or other traits to assess biodiversity  
CC and to produce other types of data and products dependent on DNA and  
CC amino acid sequences. ABG00010-ABG30377 represent novel human  
CC diagnostic amino acid sequences of the invention.  
CC Note: The sequence data for this patent did not appear in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pcl\_sequences.  
XX  
SQ Sequence 141 AA:  
  
Query Match 30.1%; Score 634; DB 22; Length 141;  
Best Local Similarity 64.3%; Pred. No. 3.5e-56;  
Matches 119; Conservative 1; Mismatches 3; Indels 62; Gaps 1;  
  
OY 178 PFEVMCDMDYRGSGWTVTQKRIDGITDFORLWCMDYLDGFGDLGFEFWLGLKRTFYVNOK 237  
DB 9 pfevmcdmdyrgsgwtvtqkridgidtgrlwcodyldgfgdl----- 51  
OY 238 NTSFMLYVALESDPTLAVASYDNFWLEDETRFRFKHNLGRYSGNAGDAFRGLKKEEDNONA 297  
DB 52 -----gdaftrglkkednampstsdvdndgcrpactlvnqgsv 66  
OY 298 MPFSTSDVDNDGCRPACLVNGOSVSKSHLHNKKTGMWFNECGLANLNGIHNEGSKLLATG 357  
DB 67 mpfstsdvdndgcrpactlvnqgsvskshlnhktgwmfnecglaingihnefsgkllatg 126  
OY 358 TOWGT 362  
DB 127 tqwgt 131  
  
RESULT 11  
ABG22361  
ID ABG22361 standard; Protein, 138 AA.  
XX  
AC ABG22361;  
XX  
DT 18-FEB-2002 (first entry)  
XX  
DE Novel human diagnostic protein #22352.  
XX  
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
KW food supplement; medical imaging; diagnostic; genetic disorder.  
XX  
OS Homo sapiens.  
XX  
PN WO200175067-A2.  
XX  
PD 11-OCT-2001.



PF		30-MAR-2001; 2001WO-US08631.	
XX			
PR		31-MAR-2000; 2000US-0540217.	
XX		23-AUG-2000; 2000US-0649167.	
XX			
PA	(HYSE-) HYSEQ INC.		
PI	Drmnac RT, Liu C, Tang YT;		
XX			
DR	WPI: 2001-639362/73.		
XX	N-PSDB; AAS86548.		
PT	New isolated polypeptide and encoded polypeptides, useful in		
PT	diagnostics, forensics, gene mapping, identification of mutations		
PT	responsible for genetic disorders or other traits and to assess		
PT	biodiversity -		
XX			
PS	Claim 20; SEQ ID NO 52720; 103pp; English.		
XX			
CC	The invention relates to isolated polynucleotide (I) and		
CC	polypeptide (II) sequences. (I) is useful as hybridisation probes,		
CC	polymerase chain reaction (PCR) primers, oligomers, and for chromosome		
CC	and gene mapping, and in recombinant production of (II). The		
CC	polynucleotides are also used in diagnostics as expressed sequence tags		
CC	for identifying expressed genes. (I) is useful in gene therapy techniques		
CC	to restore normal activity of (II) or to treat disease states involving		
CC	(II). (II) is useful for generating antibodies against it, detecting or		
CC	quantitating a polypeptide in tissue, as molecular weight markers and as		
CC	a food supplement. (II) and its binding partners are useful in medical		
CC	imaging of sites expressing (II). (I) and (II) are useful for treating		
CC	disorders involving aberrant protein expression or biological activity.		
CC	The polypeptides and polynucleotide sequences have applications in		
CC	diagnostics, forensics, gene mapping, identification of mutations		
CC	responsible for genetic disorders or other traits to assess biodiversity		
CC	and to produce other types of data and products dependent on DNA and		
CC	amino acid sequences. Abg00010-Abg30377 represent novel human		
CC	diagnostic amino acid sequences of the invention.		
CC	Note: The sequence data for this patent did not appear in the printed		
CC	specification, but was obtained in electronic format directly from WIPO		
CC	at ftp.wipo.int/pub/published_pct_sequences.		
XX			
SQ	Sequence 138 AA:		
	Query Match 29.9%; Score 628.5; DB 22; Length 138;		
	Best Local Similarity 64.6%; Pred. No. 1.2e-55;		
	Matches 126; Conservative 1; Mismatches 3; Indels 65; Gaps 1		
OY	1 MMSPEQASLPLPNCVIFICGEVVOGNCVHHSSDSSVYNIVVEGGSNAKDKSNDPYCKED 60		
Db	9 mmsplallllflnvelifvogeaqncvchbscdssvvnlvedgsnakdesksndevcked 68		
OY	61 CEESCDVTATKIREKEHFECRMIAONSIVYSTSKKLINMMDEOQASLDYLSNQNVELM 120		
Db	69 ceescdvtatkireekhfecrmlqnsivystskklirnmmdqgasldysng----- 123		
OY	121 NRVLLLTTEVERKKQLDPHPRPVQSHGLDCTDIKDITIGSVTKTPSGLYTIHREGSSYPFE 180		
Db	124 ----- 123		
OY	181 VMCDMDYRGCGWTVL 195		
Db	124 vmcgmdyrggwcvl 138		
RESULT 12			
ID ABG22364	standard; Protein; 116 AA.		
XX AC ABG22364;			
XX AC			
DT 18-FEB-2002	(first entry)		

[illegible]

XX	03-NOV-1999	(first entry)
DT	Human zapo3 protein.	
DE		
XX		
XX	Human zapo3 protein; angiotensin-1; angiotensin-2; covalently linked; moiety; affinity tag; toxin; radionuclide; enzyme; fluorophore; multimer; coiled coil domain; carboxyl-terminal fibrinogen-like domain; angiogenic; haematopoietic; mitogenic activity; angiogenesis; inhibitor; endocrine-vascular cell association; revascularisation; DNA probe; neuronal degeneration; anti-zapo3 antibody.	
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	Peptide	1..21
FT	Peptide	/label= Secretory-Signal_Sequence
FT	Peptide	43..48
FT	Peptide	/label= Immunogen
FT	Peptide	/note= "For production of antibodies"
FT	Peptide	93..98
FT	Peptide	/label= Immunogen
FT	Peptide	/note= "For production of antibodies"
FT	Peptide	120..125
FT	Peptide	/label= Immunogen
FT	Peptide	/note= "For production of antibodies"
FT	Peptide	421..426
FT	Peptide	/label= Immunogen
FT	Peptide	/note= "For production of antibodies"
FT	Peptide	422..427
FT	Peptide	/label= Immunogen
FT	Peptide	/note= "For production of antibodies"
FT	Peptide	279..490
FT	Peptide	/label= Fibrinogen-like domain
FT	Peptide	/note= "Homologous to residues 631-864 of human fibrinogen alpha chain"
FT	Peptide	63..253
FT	Peptide	/label= Amino-terminal_coiled_coil_domain
FT	Peptide	280
FT	Peptide	/note= "Conserved cysteine residue"
FT	Peptide	309
FT	Peptide	/note= "Conserved cysteine residue"
FT	Peptide	432
FT	Peptide	/note= "Conserved cysteine residue"
FT	Peptide	445
FT	Peptide	/note= "Conserved cysteine residue"
XX		
PN	W09340193-A1.	
XX		
PD	12-AUG-1999.	
XX		
PF	03-FEB-1999;	99WO-US02303.
XX		
PR	04-FEB-1998;	98US-0018258.
XX		
XX	(ZYMO ) ZYMOGENETICS INC.	
PA		
XX		
PI	Holloway JL, Shoemaker KE;	
XX		
DR	WPI: 1999-508503/42.	
XX	N-PSDB: AAX80866.	
XX		
PT	Human angiotensin homologue, ZAPo3 useful for study and regulation of angiogenesis	
XX		
PS	Claim 1; Page 65-67; 78pp; English.	
XX		
CC	The present sequence is a human zapo3 protein. Zapo3 protein exhibits significant amino acid sequence homology to angiotensin-1 and 2. It is covalently linked to a moiety chosen from affinity tags, toxins, radionuclides, enzymes and fluorophores. The protein is assembled as a multimer and is characterized by an amino-terminal coiled coil domain and a carboxyl-terminal fibrinogen-like domain. Zapo3 has angiogenic,	

Query Match	20.2%	Score 425	DB 20	Length 491
Best Local Similarity	26.9%	Pred. No. 4,1e-34		
Matches 119	Conservative 64	Mismatches 133	Indels 126	Gaps 14
QY 44	SNAAEKSRNDIVVCKEDCESCDVKTKIIR-EKHFMCMNLONSTYSYRSTKILLRNMM	102		
DB 68	tkygdastklmcltmldlenlkdvtsrqkrelvdlqldvvdgnlvnevkllkksrmm	127		
QY 103	DE-QQASLDYL-----SNQVNELMNRVLLTTE-----	129		
DB 128	srvtqlymqlhnelrkrdnslelgdenklntventemkmatryelekvysltlvp	187		
QY 130	-----VERKO-----LDB-----FRNRVOSHGI-----	148		
DB 188	ngsvmlfllaeqclrtfsrqdchvsprplvqvvrqhrlrnsqytlrqllgneqlrdpgr	247		
QY 149	DCTDlKDTIGSVTKRP-----SGXITIHPPGSSAPREV	181		
DB 248	dlmprrpdlatpsckprkrlprvtflnebrfkdcqqaekarhavsrglmlkrensgkrm	307		
QY 182	MCDMDYRGCGWVVIQKRIQIDIFORLMDYLDGFGLDGEFMLGKTKFYIVNOKNTSF	241		
DB 308	wensldpbgvewclkrtdtgsvnfflnwenyukgfgnldgwlgnlumlansqdn--y	365		
QY 242	MYVALESDDTLAYASYNFWEDETRFKMHLGRYSGNAGDAERGLKEDONAMP	301		
DB 366	kllleedvskkyuayessflerpeselfyrltlyrgnagdsimmw-----hngkqft	419		
QY 302	TSDVDNDGCRPACLVNGGVKSCSNLHNKTMGMWFNCSGLANLNGIHNSGKLLA--TGI	358		
DB 420	ldrdkd-----myagncanh-krgwmyacahsnldnrvytrgbrkshqdg	468		
QY 359	QWGTWTKNNSPVKIKSVSMKIR	380		
DB 469	fwaey--rggsyslravgmik	488		
RESULT 14				
AAV05397				
ID	AAV05397 standard; Protein: 491 AA.			
XX				
AC	AAV05397;			
XX				
DT	01-JUL-1999 (first entry)			
XX				
DE	Human TIE ligand NLS protein sequence.			
XX				
KM	Human TIE ligand; NLS; NLS; NLS; Ig homology domain; angiogenesis;			
KM	EGF homology domain; receptor tyrosine kinase; vascular endothelial cell;			
KM	early haemopoietic cell; haemopoiesis; neovascularisation; wound healing;			
KM	endothelial cell; growth inhibitor; apoptosis inducer; tumour cell;			
KM	vasculogenesis; detection; diagnosis; therapy.			
OS	Homo sapiens.			
XX				
PN	WO915653-A2.			
XX				
PD	01-APR-1999.			
XX				
PF	14-SEP-1998; 98WO-US19093.			
XX				
PR	29-OCT-1997; 97US-0960507.			

```

PR 19-SEP-1997; 97US-0933821.
XX
XX (GETH ) GENENTECH INC.
XX Botstein D, Ferrara N, Goddard A, Godowski PJ, Gurney AL;
XX Hillan K, Roy M, Schwall R, Tumas D;
XX WPI: 1999-263480/22.
DR N-PSDB; AAX36342.
XX
XX New isolated TIE ligand homologs for, e.g. developing products for
PT treatment of tumors
PS Claim 8: Fig 5: 132pp: English.
XX
XX This sequence is the human tyrosine kinase containing Ig and EGF
CC homology domains (TIE) ligand of the invention, designated NL5.
CC The TIE receptors are receptor tyrosine kinases which are expressed in
CC vascular endothelial cells and early haemopoietic cells. The TIE
CC receptors are believed to be actively involved in angiogenesis, and may
CC play a role in haemopoiesis as well. The TIE ligand homologs can promote
CC the survival and/or growth and/or differentiation of TIE receptor
CC expressing cells. They can be used for promoting neovascularisation in
CC wound healing and for promoting angiogenic processes, such as for
CC inducing collateral vascularisation in an ischaemic heart or limb, or for
CC promoting bone development and/or maturation and/or growth in a patient
CC or muscle growth and development. The TIE ligand homologs and antibodies
CC can inhibit the growth of endothelial cells and induce apoptosis of
CC cells, particularly tumour cells. They can inhibit vasculogenesis,
CC particularly the vascularisation of tumour cells. The antibodies can also
CC inhibit vascularisation of a cell in which a gene encoding an NL1, NL5,
CC NL8 or NL4 polypeptide is amplified. The products can also be used for
CC detection, diagnosis, drug screening and production of transgenic
CC animals.
XX
XX Sequence 491 AA:
SQ

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RESULT 15
AAB24393
ID AAB24393 standard; Protein; 491 AA.
XX
XX AAB24393;
AC
XX
XX 07-NOV-2000 (first entry)
DT
XX
XX Human PRO188 protein sequence SEQ ID NO:26.
DE
XX
XX Human: PRO: promotion; inhibition; angiogenesis; cardiovascularisation;
KW diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy;
KW angiogenic; proliferative; cardiac; cardiovascular; antiatherosclerotic;
KW cytosolic; gene therapy; vaccine.
XX
XX Homo sapiens.
XX
XX WO200032221-A2.
PN
XX
XX 08-JUN-2000.
PD
XX
XX 30-NOV-1999; 99WO-US28313.
XX
XX 01-DEC-1998; 98WO-US25108.
PR 16-DEC-1998; 98US-0112850.
PR 12-JAN-1999; 99US-0115554.
PR 08-MAR-1999; 99WO-US05028.
PR 12-MAR-1999; 99US-0123957.
PR 28-APR-1999; 99US-0131445.
PR 14-MAY-1999; 99US-0134287.
PR 02-JUN-1999; 99WO-US12252.
PR 23-JUN-1999; 99US-0141037.
PR 20-JUL-1999; 99US-0144758.
PR 26-JUL-1999; 99US-0145698.
PR 01-SEP-1999; 99WO-US20111.
PR 08-SEP-1999; 99WO-US20594.
PR 13-SEP-1999; 99WO-US20944.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 05-OCT-1999; 99WO-US23089.
PR 29-OCT-1999; 99US-0162506.
XX
XX (GETH ) GENENTECH INC.
XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Hillan KJ, Goddard A;
XX Godowski PJ, Gurney AL, Klein RD, Kuo SS, Paoletti NF, Smith V;
XX Watanabe CK, Williams PM, Wood WI.
XX
XX WPI: 2000-412154/35.
DR N-PSDB; AAA77529.
XX
XX Nucleic acids encoding PRO polypeptides useful for preventing,
PT diagnosing and treating disorders of a cardiovascular, endothelial or
PT angiogenic disorders in mammals -
XX
XX Claim 72: Fig 12: 315pp: English.
XX
XX The present invention describes nucleic acids encoding PRO polypeptides
XX useful for preventing, diagnosing and treating disorders in mammals by
XX cardiovascular, endothelial or angiogenic disorder in mammals by
XX modulating cell proliferation, angiogenesis and cardiovascularisation,
XX and for identifying agonists and antagonists of these processes. The
XX nucleic acids and the proteins they encode may be used in the
XX prevention, treatment and diagnosis of diseases associated with
XX inappropriate PRO expression such as cardiovascular, endothelial or
XX angiogenic disorders in mammals (e.g. atherosclerosis, cancers and
XX cardiac hypertrophy). For example, the nucleic acids (NAs) and vectors
XX containing them and the PRO polypeptide may be used to treat disorders
XX associated with decreased PRO expression. AAA77510 to AAA77721 and
XX AAB24388 to AAB24435 represent nucleotide and protein sequences used in
XX the exemplification of the present invention.

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Db	128	SRVQLVQLLHEIIRKRDNSLELSQENKILANTTEMILKATRYRELEKAYASLDLVN	187
QY	130	-----VRRKQ---LDP-----FRRPVQSHGL-----	148
Db	188	NQSWMTLLLEECRLRFSRODHTNSPRLVQVVRPHNIENSOQYRRPGLGNEIORDPGR	247
QY	149	DCDILKQIIGSVTKTP-----	161
Db	248	DLMPRPDLPTSPKSPKIPRPVTEINEGRPKDQQAKEAGHSVSGIYMKPENSNGPQL	307
QY	182	MCDMDYRGCGVTVQIKRIDGIIDFQRLMCDVLDLDFGDLGFEMLKRIYVIMQKTSF	241
Db	308	WCENSLDRPGMTVQIKRIDGVSVNFRRMKNENTKKGFQINIDGFTYGLGLENITMLSQDN--Y	365
QY	242	MLVVALESEDITLVAASYDNFMLEDETEFFFKMIGRGYSGNAGDAFRGLAKEDNONAMPFS	301
Db	366	KLLLELEDMDSKKYVAEVSFRLEPESFPYLRIGTYQGNAGDSMM-----HNCKQFT	419
QY	302	TSVDVNDGCRAPACLIVNGOSVKSCHLHNKTKGMFNECGLANLNGIHHFSGKLLA---TGI	358
Db	420	TLDRLDKD-----MYAGNCAPHN-KFGGMWYNACASHNLNGLVWYRGCHYRSKHODGI	468
QY	359	QMGMTKNNSPVKIKSVSMKR 380	
Db	469	FMAEY--RGGSYSLRAVQMMTK 488	

RESULT 2  
 US-08-960-507-4  
 Sequence 4, Application US/08960507  
 Patent No. 6057435  
 GENERAL INFORMATION:  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Gurney, Austin L.  
 TITLE OF INVENTION: The Ligands  
 NUMBER OF SEQUENCES: 24  
 CORRESPONDENCE ADDRESSES:  
 ADDRESSEE: Genentech, Inc.  
 STREET: 1 DNA Way  
 CITY: South San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94080  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: WinPatIn (Genentech)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/960.507  
 FILING DATE:  
 CLASSIFICATION: 536  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Dreyer, Ginger R.  
 REGISTRATION NUMBER: 33,055  
 REFERENCE/DOCKET NUMBER: P1130p1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 650/225-3216  
 TELEFAX: 650/952-9881  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 491 amino acids  
 TYPE: Amino Acid  
 TOPOLOGY: Linear  
 US-08-960-507-4

	Query Match	20-28;	Score 425;	DB 3;	Length 491;
	Best Local Similarity	26.9%;	Pred. No. 1e-35;		
	Matches 119; Conservative	64;	Mismatches 133;	Indels 126;	Gaps 14;
QY	44 SNAKESNDIVCEDEECSDVATKTIRE-EKHFMCNLTNSIVSTRSTKLLRNMM	102			
	:   :   :   :     :   :	:	:	:   :	:

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Db      68  TKGDASTIKMILTRMDLENKDYLSNQKREIDVLQVVDGIVNEVYLLKRESNNM 127
QY      103  DE-QQASIDLVL-----SNQVNEIMNRVLLTTT----- 129
Db      128  SRVQLVWQLLHEIIRKRDNSLELSQENKILNVTEMKMATRYRELEVAYASTDLVN 187
QY      130  -----VERKQ---LDP-----PFRPVQSHGL----- 148
Db      188  NQSVMTLLEBQCLRIEFSRODTHVSPRYLVQVVRQNIINPSQUTYRGLLGGNEIORDPGR 247
QY      149  DCTDIKDTIGSVYTP-----SGLYIHPBESSIPFEV 161
Db      248  DLMPPRLDATSPTKSPKIPRVPTFINEGRPKDCQAKESCHSVSGIATYMKIPENSNGPMQL 307
QY      182  MCDMDYRGGGVTYQKRLDGIIDQRLMCDYLDGFGDLSEFYLGLKITYYVNOKQTSF 241
Db      308  WCENSELDPGGGVTYQKRTDGSVNFEEFRMWNENYKQFGNIDDEYWLGLENIYMLSNOD--Y 365
QY      242  MLYVALESEDOTLAVASVDNFMLEDEDFRFRMHLGRSGNAGQAFRLKKEDONAMPFS 301
Db      366  KLLIELEWDSOKKYVAEYSSFRLESESEFYRLRIGTYQAGNAGSMW-----HNGKQPT 419
QY      302  TSDVDNDCRPACLVNGQSVYSCSHLNNKTCGMWNEEGCLANLUNGIIHFSGLKLA--TGI 358
Db      420  TLDLRDKD-----MYAGNCNHFH-KGGWMTNACASHSLNGLNVYRGCHYRSKHODGI 468
QY      359  QMGTYTKNNSPVKIKSVSMKIR 380
Db      469  FWAEY--RGGSYSILRAVOMMIK 488

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Query Match	20.28;	Score 425;	DB 4;	Length 491;
Best Local Similarity	26.98;	Pred. NO. 1e-35;		

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1 RESULT 4
2 US-08-740-223A-12
3 ; Sequence 12, Application US/08740223A
4 ; Patent No. 6263564
5 ;
6 ; GENERAL INFORMATION:
7 ; APPLICANT: Davis, et al.
8 ; TITLE OF INVENTION: Expressed Ligand - Vascular
9 ; TITLE OF INVENTION: Intercellular Signalling Molecule
10 ; NUMBER OF SEQUENCES: 28
11 ;
12 ; CORRESPONDENCE ADDRESS:
13 ; ADDRESSEE: Regeneron Pharmaceuticals, Inc.
14 ; STREET: 777 Old Saw Mill Road
15 ; CITY: Tarrytown
16 ; STATE: NY
17 ; COUNTRY: USA
18 ; ZIP: 10591
19 ;
20 ; COMPUTER READABLE FORM:
21 ; MEDIUM TYPE: Diskette
22 ; COMPUTER: IBM Compatible
23 ; OPERATING SYSTEM: DOS
24 ; SOFTWARE: FastSeq Version 2.0
25 ;
26 ; CURRENT APPLICATION DATA:
27 ; APPLICATION NUMBER: US/08/740,223A
28 ; FILING DATE: 25-OCT-1996
29 ; CLASSIFICATION: 536
30 ;
31 ; PRIOR APPLICATION DATA:
32 ; APPLICATION NUMBER: USSN 60/022/999
33 ; FILING DATE: 02-AUG-1996
34 ;
35 ; ATTORNEY/AGENT INFORMATION:
36 ; NAME: Cobert, Robert J
37 ; REGISTRATION NUMBER: 36,108
38 ; REFERENCE/DOCKET NUMBER: REG 333
39 ;
40 ; TELECOMMUNICATION INFORMATION:
41 ; TELEPHONE: 914-345-7400
42 ; TELEFAX: 914-345-7721
43 ;
44 ; INFORMATION FOR SEQ ID NO: 12:
45 ; SEQUENCE CHARACTERISTICS:
46 ; LENGTH: 490 amino acids
47 ;

```

Query Match	19.3%	Score 405.5;	DB 4;	Length 490;
Best Local Similarity	27.5%;	Pred. No. 1.1e-33;		
Matches 118; Conservative	65;	Mismatches 125;	Indels 121;	Gaps 16

```

1  RESULT# 5
2  US-08-740-223A-4
3  ; Sequence 4, Application US/08740223A
4  ; Patent No. 6265564
5  ; GENERAL INFORMATION:
6  ; APPLICANT: Davis, et al.
7  ; TITLE OF INVENTION: Expressed Ligand - Vascular
8  ; TITLE OF INVENTION: Intracellular Signalling Molecule
9  ; NUMBER OF SEQUENCES: 28
10 ; CORRESPONDENCE ADDRESS:
11 ; ADDRESSEE: Regeneron Pharmaceuticals, Inc.
12 ; STREET: 777 Old Saw Mill Road
13 ; CITY: Tarrytown
14 ; STATE: NY
15 ; COUNTRY: USA
16 ; ZIP: 10591
17 ; COMPUTER READABLE FORM:
18 ; MEDIUM TYPE: Diskette
19 ; COMPUTER: IBM Compatible
20 ; OPERATING SYSTEM: DOS
21 ; SOFTWARE: FastSeq Version 2.0
22 ; CURRENT APPLICATION DATA:
23 ; APPLICATION NUMBER: US/08/740,223A
24 ; FILING DATE: 25-OCT-1996
25 ; CLASSIFICATION: 536
26 ;

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OY 372 IKSYSMKIR 380  
Db 485 LRSTTMMIR 493

## RESULT 7

US-08-418-595-4  
; Sequence 4, Application US/08418595  
; Patent No. 5814464  
; GENERAL INFORMATION:  
; APPLICANT: Davis, et al.  
; TITLE OF INVENTION: TIE-2 LIGAND, METHOD OF MAKING AND USES  
; TITLE OF INVENTION: THEREOF  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Regeneron Pharmaceuticals, Inc.  
; STREET: 777 Old Saw Mill River Road  
; CITY: Tarrytown  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10591  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/418,595  
; FILING DATE: 06-APR-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/373,579  
; FILING DATE: 17-JAN-1995  
; APPLICATION NUMBER: US 08/353,503  
; FILING DATE: 09-DEC-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/348,492  
; FILING DATE: 02-DEC-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/330,261  
; FILING DATE: 27-OCT-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/319,932  
; FILING DATE: 07-OCT-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Cobert, Robert J.  
; REGISTRATION NUMBER: 36,108  
; REFERENCE/DOCKET NUMBER: REG 330-D  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (914) 345-7400  
; TELEFAX: (914) 345-7721  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 497 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-418-595-4

Query Match 19.1%; Score 402.5; DB 2; Length 497;  
Best Local Similarity 27.3%; Pred. No. 2.3e-33;  
Matches 117; Conservative 66; Mismatches 125; Indels 121; Gaps 16;

OY 23 VQNCVHHSTDSVYNIVEDGSKNAKDESKSNDTVCKEDCESCDVKRTITREKHFMCRN 82  
Db 115 IQQNAVQNHNT-----ATMLEIGTSLISQ-----ABQTRKRLDVEVQVLNQTSLRIQL 163  
OY 83 LQNSIVS-----TRSTKRLLRMM 102  
Db 164 LENSLSYTKLEKOLLQOTNELIKIHKNSLLEHRIEMEGKHKRELDLTLEKEKENLOGLV 223

OY 103 DEQASLDYLSNOVN-----ELM-----NRVLLTTEVE-----RKOLDPEP 139  
Db 224 TRQTYIIQLELEKOLNRAFTNNSVLQKQOELMDVHNLNCTKEVLLKGKREDEPF- 282  
OY 140 HRPVQSHGLDCTDIKDTIGSVTKTPSGLYIHPGSSYPFEVWCDMDYRGQGWTVIOKRI 199  
Db 283 -----RDCADYV-----QAGFNKSGIYTYIINMPEPKKVFNCMDVNGGQWTVIOHRE 330  
OY 200 DGIIDFQRLMCDYLDGFGDGLGEFWMGLKTFEYVYNQKNSFMILYVALLSEDDTLAVASY 259  
Db 331 DGSIDFQRMKEYMGFGNPSGEYWLGNFTFATTSQ--QYMLRIELMDGGRAYSOY 388  
OY 260 DNFMLEDETRFKMHLGRYSNAGDAFRGLKEEDN--QMAPFSTSDVNDGCRPAC--TL 315  
Db 389 DRFHIGNEKQYRXLXGHTAG-----KQSSLIHGADFSTKADNDNCCKKCALM 441  
OY 316 VNGQSVXSCSHLHNTGWMFNEGLANLNGIHRS---GKLATGIGQWGTWTRKNSPVK 371  
Db 442 LTG-----GWMFDACGPNLNGMFTYAGQNHGKL--NGIKMHYF--KGRSYS 484  
OY 372 IKSYSMKIR 380  
Db 485 LRSTTMMIR 493

## RESULT 8

US-08-665-926-4  
; Sequence 4, Application US/08665926  
; Patent No. 5851797  
; GENERAL INFORMATION:  
; APPLICANT: Valenzuela et al.  
; TITLE OF INVENTION: TIE LIGAND-3, METHODS OF MAKING AND USES  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Regeneron Pharmaceuticals, Inc.  
; STREET: 777 Old Saw Mill River Road  
; CITY: Tarrytown  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10591-6707  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/665,926  
; FILING DATE: 19-JUN-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Robert J. Cobert  
; REGISTRATION NUMBER: 36,108  
; REFERENCE/DOCKET NUMBER: REG 330-H  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (914) 345-2113  
; TELEFAX: (914) 345-7400  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 497 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-665-926-4

Query Match 19.1%; Score 402.5; DB 2; Length 497;  
Best Local Similarity 27.3%; Pred. No. 2.3e-33;  
Matches 117; Conservative 66; Mismatches 125; Indels 121; Gaps 16;

OY 23 VQNCVHHSTDSVYNIVEDGSKNAKDESKSNDTVCKEDCESCDVKRTITREKHFMCRN 82  
Db 115 IQQNAVQNHNT-----ATMLEIGTSLISQ-----ABQTRKRLDVEVQVLNQTSLRIQL 163



FILING DATE: 09-DEC-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/348,492  
FILING DATE: 02-DEC-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/330,261  
FILING DATE: 27-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/319,932  
FILING DATE: 07-OCT-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Coberl, Robert J.  
REGISTRATION NUMBER: 36,108  
REFERENCE/DOCKET NUMBER: REG 330-D  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (914) 345-7400  
TELEFAX: (914) 345-7721  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 497 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-162-437-4

Query Match 19.1%; Score 402.5; DB 4; Length 497;  
Best Local Similarity 27.3%; Pred. No. 2,3e-33;  
Matches 117; Conservative 66; Mismatches 125; Indels 121; Gaps 16;

23 VQNCVHHSTDSVNIIVDGSNAKDESKNDVCEDESCDVYKTRREKHPMCRN 82  
115 IQQNAVQNT-----ATMEIGTSLSQT-----AEQTRKLDVETQVLYNQTSLREID 163  
83 LQNSIVSY-----TSTTKILLRNMA 102  
164 LENSISTYKLEKQLDQOTNEILKHEKNSLLEKILMEGKHKEELDTLKEEKENGLV 223  
103 DQOASLDVLSQNV-----ELM-----NRVLLLTTFE-----RKQIDPPR 139  
224 TQOTYIIQLEKQLNATNTNSVLOKQOLEMDTVNLVNLCTKEVLLKGKREEDKPF- 282  
140 HRPVOSHGLDCTDIKDTIGSVTTPSGLYIHPGSSYFEVMDYRGSGWTYQKRI 199  
283 -----RDCAADV-----QAGFNKSGITTYIINNMPERKAFPCNDVAGGCTVYQHNE 330  
200 DGIIDFQRLMCDYLDGEGDLLEFWLGLKRFIYVNOKNTSFMLYVALESEDDTLAYASY 259  
331 DGLDFQRCMKREYKMGFGNPGEYWLGNFEIFAITSOR--QYMLRIELMDWEGNRAVSQY 388  
260 DNEWLEDERFRFKMHLGRYSNAGDAFRGLKEDN--QNAAPFSTDVDVNDGCRPAC--L 315  
389 DRFHIGNEKQNRLYLKGTGTAG-----KQSSLILHGADESTKDADNDCMCKCALM 441  
316 VNGOSVKSCHLHNKTMFNEGCLANLNGIHHSF---GKLLATGIGQGTWTKNNSPVK 371  
442 LRG-----GWFDAQCGPSNLMGMFTYTAGNNGKL--NQIKKHVF--KQPSYS 484  
372 IKSVMKIR 380  
485 LRSTWIR 493

RESULT 11  
US-08-933-821-2  
Sequence 2, Application US/08933821  
Patent No. 5972338  
GENERAL INFORMATION:  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
TITLE OF INVENTION: Tie Ligands  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/933,821  
FILING DATE:  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Dreger, Ginger R.  
REGISTRATION NUMBER: 33,055  
REFERENCE/DOCKET NUMBER: P1130  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-3216  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 493 amino acids  
TYPE: Amino Acid  
TOPOLOGY: linear  
US-08-933-821-2

Query Match 19.0%; Score 400; DB 2; Length 493;  
Best Local Similarity 31.9%; Pred. No. 4,2e-33;  
Matches 94; Conservative 50; Mismatches 93; Indels 58; Gaps 11;

117 NELMNRVLLLTTEVFRKQ-----LDPFRRPVQSHGLDCTDIKDTIGSVTKTPSG----- 166  
231 NRIINQI--STNEIQSDQMLKVLPLPLPTMTLT-----SLPSSTDKPSGWRDC 278  
167 -----LYIHPGSSYFEVMDMDYRGSGWTYQKRIIDFQRLMCDYLD 214  
279 LQALEDHDTSSYLVKRPENTNRLMQWCDQRDPGQVTVIORLDGVSYFRMMEYKQ 338  
215 GFEDLLDEFMLGLKRFIYVNOKNTSFMLYVALESEDDTLAYASVNFLEDETRFKMH 274  
339 GFGNDIGETVWLGLENTYWLTLQGN--YKLLVTMEDMSGKRVRAEYASFLEPSEYKIR 396  
275 LGRYSNAGDAFRGLKEDNQNAMPFSTDVDNDGCRPACLVNGOSVKSCHLHNKTMW 334  
397 LGRHYNAGDSFTW-----HNGKQFTTLDRIHD-----VYTG--NCAH-YQKGWM 439  
335 FNEGCLANLNGIHHSQKLLA---TGIONGTWTKNNSPVKIKSVSKIRMTNPNY 386  
440 YNACAHSNLNGVWYRGHYRSRYQGVYAEF--RGGSYSLKRVYVMIRPNPTF 492

RESULT 12  
US-08-960-507-2  
Sequence 2, Application US/08960507  
Patent No. 6057435  
GENERAL INFORMATION:  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
TITLE OF INVENTION: Tie Ligands  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk



```

; FILING DATE: 23-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: OHLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 4587-012-0 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ. ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 312 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-525-505A-4

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Query Match 19.0%; Score 399; DB 1; Length 312;
Best Local Similarity 34.3%; Pred. No. 2.6e-33;
Matches 111; Conservative 44; Mismatches 115; Indels 54; Gaps 12;

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QY 87 IVSTSTKRLKLNMDDEQASLDYLSNOYNEIMNRYLLITTEVERKQ-----134
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 4 VFSFLLVTTALLI--MGREISALEDCAQEQMRRAQVRLLETRVKQOQVXIKOLLQENLV 60
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 135 --LDPPPHRPVQSHG-----LDCTDIKDTIGSVTKTPSGLYIIHPRESSYPRFWMQMDY 167
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DB 61 QFLDKGDENTVDLGSRKQYADCSLFDGCKL-----SGFYKTKLPQSPAEFSYCDMS- 115
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QY 188 RGGGWTVYIQKRIDGIIDFQRLMCDYLDGFGDL--GEFWLGLKIFYIVNOKNTSEMLY 244
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 116 DGGGWTVYIQKRSDGSEFNKMGWYDENGFGNFYQKHGEYVLGNKLNHLFTQED--YTLK 173
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 245 VALESDDTAYASYNDFWLEDETREFPKMHLGRYSGNAGAFGLKKEDNQ-----NAMP 299
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 174 IDLADEKKNRYAQKFKFKYDDEKNFEYELNIGESGTAGSLAGNPFHEVQWMAASHQRMK 233
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 300 FSTSDVNDQCRPACLYNGSVKSCSHLNKGMFNEGCLANLNGIHHSGLKLA--T 356
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 234 FSTWDRDHDYEGNCAEEDS-----GWFENRCHSANLNGV--YISGPYTAKTDN 281
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 357 GIOMGTWTKNNSPVKIKSVSMKIR 380
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 282 GIWWTW--HGMWYSLKSVYMKIR 303
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

RESULT 15
US-08-740-223A-22
; Sequence 22, Application US/08740223A
; Patent No. 6265564
; GENERAL INFORMATION:
; APPLICANT: Davis, et al.
; TITLE OF INVENTION: Expressed Ligand - Vascular
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Regeneron Pharmaceuticals, Inc.
; STREET: 777 Old Saw Mill Road
; CITY: Tarrytown
; STATE: NY
; COUNTRY: USA
; ZIP: 10591
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/740,223A
; FILING DATE: 23-OCT-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 60/022/999

```

```

; FILING DATE: 02-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Cobert, Robert J
; REGISTRATION NUMBER: 36,108
; REFERENCE/DOCKET NUMBER: REG 333
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 914-345-7400
; TELEFAX: 914-345-7721
; INFORMATION FOR SEQ. ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 496 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: Internal
; FEATURE:
; NAME/KEY: 2N2C1F (chimera 2)
; LOCATION: 1...496
; OTHER INFORMATION:
; US-08-740-223A-22

```

```

Query Match 18.8%; Score 395.5; DB 4; Length 496;
Best Local Similarity 27.5%; Pred. No. 1.2e-32;
Matches 116; Conservative 68; Mismatches 133; Indels 105; Gaps 17;

```

```

QY 23 VQNCVHHSTDSVSVNIVEDGNSNAKDESKNDYVCKEDCESCDVTKT-----TREE--- 75
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 112 IQONAAVQNT-----AVWIEIGTNLNTOT-----AEQTRKLDVEAQVNLNTTRELQL 160
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 76 -KHFMGN-LQNSIVSYTRSTKTL-----AEQTRKLDVEAQVNLNTTRELQL 109
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 161 LEHSLSTNKLKQIQLDTSINKLQDKNSFLKLVAMBDKHITQLQSIKEKQDQLVLY 220
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 110 DYLSNOYNEIMNRYLLIT--TEVERKQ-----LDPPPHRPVQSH 146
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 221 SKNSIIELEKKIVTATVANSVLQKQHDIMETVNNLLTMSTNSAKRPTVAKKEQIS 280
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 147 GLDCTDIKDTIGSVTKTPSGLYIIHPGSSYPREVMQMDYRGCGWTVYQKRIDGIIDFQ 206
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 281 FRCDADYV---OAGFNKSGIYIYINNMPKPKVFCNMDVNGSGWTVYQHRDGSIDFQ 336
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 207 RLMCDYLDGFGDLGGEFWLGLKIFYIVNOKNTSEMLYVALESBDPLTAYASYNDFWLED 266
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 337 RGMKEYKMGFNPSEGEYWLGNFEIITTSOR--QIMRLTLMDEGNRAVSQYDRFHIGN 394
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 267 ETRFEKMHLLGRYSGNAGDAFRGLKKEDN--QNAPEFSTSDVDNDGCRPAC--LVNGOSVK 322
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 395 EKQYRRLXKLKGHTAG-----KQSSLLHGADFSTKADNDNCMKCALMLTG----- 443
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 323 SCSHLNKGTWNEGCLANLNGIHHS---GKLATGIGOMGTWTKNNSPVKIKSVSMK 378
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 444 -----GWFEDACPSNLNGWFTYAGONHGKL--NGIKMYF--KGPSYSLRSTYTM 490
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 379 IR 380
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 491 IR 492
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

Search completed: May 22, 2002, 15:07:54  
Job time: 166 sec

**This Page Blank (uspto)**

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 22, 2002, 15:13:50 ; Search time 17.4 Seconds

(without alignments)  
818.896 Million cell updates/sec

Title: US-09-596-196-9  
Perfect score: 2000  
Sequence: 1 EVVQGNCHVHSTDSVYVNTV.....PVKIKSVSMKIRMYNPFYK 368

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 105224 segs, 38719550 residues  
Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	413.5	20.7	439	1	FGL2_HUMAN
2	405.5	20.3	432	1	FGL2_MOUSE
3	400.5	20.0	481	1	AGP1_BOVIN
4	400.5	20.0	493	1	ANL2_MOUSE
5	400.5	20.0	493	1	ANL2_HUMAN
6	398	19.9	312	1	FGL1_HUMAN
7	395.5	19.8	468	1	FIBB_BOVIN
8	395	19.6	498	1	AGP1_HUMAN
9	391	19.1	496	1	AGP2_MOUSE
10	381.5	18.8	491	1	FIBB_HUMAN
11	375.5	18.8	375	1	AGP2_BOVIN
12	375	18.7	496	1	AGP2_MOUSE
13	373.5	18.7	479	1	FIBB_RAT
14	371.5	18.6	463	1	FIBB_CHICK
15	370	18.5	477	1	FIBB_PETMA
16	367.5	18.4	453	1	FIBG_BOVIN
17	365	18.2	444	1	FIBG_BOVIN
18	360	18.0	432	1	FIBG_PETMA
19	360	18.0	509	1	AGP4_MOUSE
20	358	17.9	503	1	AGP4_HUMAN
21	352.5	17.6	438	1	FIBG_XENLA
22	351	17.6	319	1	FCN2_RAT
23	350.5	17.5	282	1	FIBB_PARPA
24	348.5	17.4	774	1	SCA_DROME
25	337.5	16.9	866	1	FIBA_HUMAN
26	335	16.8	741	1	FIBB_CHICK
27	332	16.6	306	1	FCN2_MOUSE
28	329.5	16.5	641	1	FIB2_PETMA
29	329	16.4	334	1	FCN1_MOUSE
30	327.5	16.4	445	1	FIBG_RAT
31	321.5	16.1	313	1	FCN2_HUMAN
32	321	16.1	255	1	MFA4_HUMAN

34	313.5	15.7	782	1	FIBA_RAT	P06399
35	310.5	15.5	1808	1	TENA_CHICK	rattus norv
36	305.5	15.3	335	1	FCN1_RAT	P10039
37	303.5	15.2	326	1	FCN1_HUMAN	gallus gall
38	302.5	15.1	4289	1	TENX_HUMAN	O9wts8
39	291	14.6	299	1	FCN3_HUMAN	rattus norv
40	282.5	14.1	1746	1	TENA_PIG	P22105
41	271	13.6	2201	1	TENA_HUMAN	homo sapien
42	197	9.8	137	1	AGP2_RAT	O75636
43	109	5.5	129	1	AGP2_BOVIN	homo sapien
44	98	4.9	782	1	MFA4_BOVIN	Q29116
45	97.5	4.9	1432	1	SKI3_YEAST	homo sapien

## ALIGNMENTS

RESULT 1  
FGL2\_HUMAN FGL2\_HUMAN STANDARD: PRT; 439 AA.  
ID FGL2\_HUMAN Q14314  
AC Q14314  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Fibrinogen-like protein 2 (P149).  
GN FGL2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Small intestine;  
RX MEDLINE=95369700; PubMed=7642106;  
RA Ruegg C., Pytela R.;  
RT "Sequence of a human transcript expressed in T-lymphocytes and encoding a fibrinogen-like protein."  
RL Gene 160:257-262(1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Yuvaraj S., Liu M., Marsden P., Levy G.;  
RT "Cloning and characterization of HFG2, the human counterpart to the mouse gene Fgln2."  
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP CHARACTERIZATION:  
RX MEDLINE=98309432; PubMed=9647217;  
RA Marazzi S., Blum S., Hartmann R., Gundersen D., Schreyer M.,  
RA Arraraves S., von Fliedner V., Pytela R., Rugg C.;  
RT "Characterization of human fibrinogen, a fibrinogen-like protein secreted by T lymphocytes."  
RL J. Immunol. 161:1138-147(1998).  
CC -1- FUNCTION: MAY PLAY A ROLE IN PHYSIOLOGIC LYMPHOCYTE FUNCTIONS AT MUCOSAL SITES.  
CC -1- SUBUNIT: HOMOTETRAMER; DISULFIDE-LINKED.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: CONSTITUTIVELY EXPRESSED IN CYTOTOXIC T-CELLS.  
CC -1- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.  
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CC EMBL: Z65331, CA85298.1, -;  
CC EMBL: AF104015, AADI0825.1, -;  
CC EMBL: AF104014, AADI0825.1, JOINED.  
CC HSSP: P02671, 1F2D.  
CC MW: 605351, -;





Db 363 -----NCG-LYSSGWFSDCLSANLNGKYYHKKYKGVNRCIFWGTGPGINQAPGGYKS 416  
 QY 355 VSMKIRRMNP 365  
 Db 417 SFOAKMMIRP 427

RESULT 3  
 AGPL\_BOVIN STANDARD; PRT; 481 AA.  
 ID AGPL\_BOVIN  
 AC 018920;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Angiopoietin-1 precursor (ANG-1) (Fragment);  
 GN ANGPT1 or ANG1.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OC NCBI\_TaxID=9913;  
 OX  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Ovary;  
 RX MEDLINE=99054348; PubMed=9840613;  
 RA Goede V., Schmidt T., Klimina S., Kozian D., Augustin H.G.;  
 RT "Analysis of blood vessel maturation processes during cyclic ovarian  
 angiogenesis";  
 RL Lab. Invest. 78:1385-1394(1998).  
 RN [2]  
 RP SEQUENCE OF 91-200 FROM N.A.  
 RC TISSUE-liver;  
 RX MEDLINE=98451564; PubMed=9776732;  
 RA Mandriota S.J., Pepper M.S.;  
 RT "Regulation of angiopoietin-2 mRNA levels in bovine microvascular  
 endothelial cells by cytokines and hypoxia";  
 RL Circ. Res. 83:852-859(1998).  
 CC  
 CC -1- FUNCTION: BANDS AND ACTIVATES TIE2 RECEPTOR BY INDUCING ITS  
 TYROSINE PHOSPHORYLATION. IMMEDIATELY IN ENDOTHELIAL DEVELOPMENTAL/  
 PROCESSES LATER AND DISTINCT FROM THAT OF VEGF. APPEARS TO PLAY A  
 CRUCIAL ROLE IN SURROUNDING RECIPROCAL INTERACTIONS BETWEEN THE  
 ENDOTHELIUM AND SURROUNDING MATRIX AND MESENCHYME. MEDIATES BLOOD  
 VESSEL MATURATION/STABILITY. IT MAY PLAY AN IMPORTANT ROLE IN THE  
 HEART EARLY DEVELOPMENT (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- DEVELOPMENTAL STAGE: FOUND TO BE EXPRESSED THROUGHOUT THE OVARIAN  
 CYCLE.  
 CC -1- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.  
 CC  
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 or send an email to [license@sb-sib.ch](mailto:license@sb-sib.ch)).  
 CC  
 CC EMBL: AF093573; AAC61872.1; -  
 DR EMBL: AF032923; AAC78245.1; -  
 DR HSSP: P02671; LF2D.  
 DR InterPro: IPR002181; Fibrinogen\_C.  
 DR Pfam: PF00147; fibrinogen\_C; 1.  
 DR SMART: SM00186; FRG: 1  
 DR PROSITE: PS00514; FIBRIN-AG\_C-DOMAIN; 1.  
 KW Glycoprotein; Coiled coil; Signal.  
 FT SIGNAL 1 15  
 FT CHAIN 16 >481 POTENTIAL.  
 FT DOMAIN 153 >261 ANGIOPOIETIN-1.  
 FT DOMAIN 283 >481 COILED COIL (POTENTIAL).  
 FT CARBOHYD 92 >481 FIBRINOGEN C-TERMINAL.  
 FT CARBOHYD 122 122 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 154 122 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 243 243 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 294 294 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT NON\_TER 481 481  
 SO SEQUENCE 481 AA; 55556 MW; 8EEC9ED84FC2BB50 CRC64;  
 Query Match 20.0%; Score 400.5; DB 1; Length 481;  
 Best Local Similarity 27.9%; Pred. No. 1,1e-24;  
 Matches 114; Conservative 60; Mismatches 116; Indels 119; Gaps 15;  
 QY 3 VQNCVHHSTDSVNVNIVEDSGSNMADESKSNDTYCKEDCESDVKTKITREKHFMCRN 62  
 Db 115 IQQNAVQNHNT-----ATMLEIGTSLLSQT-----AEOTRKLTDETQVLTNQTSLRIQL 163  
 QY 63 LQNSIVSY-----TRSKKLLRMNM 82  
 Db 164 LENSLSITYKLEKOLLQQTNEILKHEKNSLLEHKLFEKEGKHELDLTKEKEKLEGLQV 223  
 QY 83 DEQQASLDYLSNOVN-----ELM-----NVLTLTTEVF-----RKQLDPP 119  
 Db 224 TRQTYIIQLELEKQLNRATNNSVLQKQDELMDYHNLVNLCTKRVLLKGGKREKPEF- 282  
 QY 120 HRPVQSHGLDCTDIKDTIGSVTKTPSGLYIHPGSSYPFVEYCDMDYRGGMVYQKRI 179  
 Db 283 -----RDCADVY-----QAGFNKSGITYTYIYINMPEPKVKYFCMDLNGGWTYIOHRE 330  
 QY 180 DGIIDFORLMDYLDGFGDDLGEFVLGUKTFYINQKNTSMXLYVALESEDDTLATVASY 239  
 Db 331 DGSIDFORGMKRYKGFNPSEYWLGNPFALTSQY--QYTLIELLDWGNRAYSOY 388  
 QY 240 DNFWEDETRFFKMLHGRYSGNAGDAFRLKKEKN--GNAMFSTSDVNDGCRPAC--L 295  
 Db 389 DRFHIGNEKQNRILYLRKHTGTAG-----KQSSLLHAGDFSTKDDNDNCKMKCALM 441  
 QY 296 VNGQSVKSCSHLHNTGWMFNECGLANINGHNS-----GKLLATGICW 340  
 Db 442 LTG-----GWMFDACGSPNMGMYTAGQNHKGL--NGIKW 475  
 RESULT 4  
 ANL2\_MOUSE STANDARD; PRT; 493 AA.  
 ID ANL2\_MOUSE  
 AC 09R045;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 01-MAR-2002 (Rel. 41, Last annotation update)  
 DE Angiopoietin-related protein 2 precursor (Angiopoietin-like 2).  
 GN ANGPTL2 OR ARP2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Heart;  
 RX MEDLINE=99403103; PubMed=10473614;  
 RA Kim I., Moon S.-O., Koh K.N., Kim H., Uhm C.-S., Kwak H.J., Kim N.-G.,  
 RA Koh G.Y.;  
 RT "Molecular cloning, expression, and characterization of angiopoietin-  
 related protein. angiopoietin-related protein induces endothelial cell  
 sprouting";  
 RL J. Biol. Chem. 274:26523-26528(1999).  
 CC -1- FUNCTION: INDUCES SPROUTING IN ENDOTHELIAL CELLS THROUGH AN  
 AUTOCRINE AND PARACRINE ACTION (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).  
 CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED IN HEART, TONGUE, LUNG AND  
 SKELETAL MUSCLE. ALSO FOUND IN LOWER LEVELS IN KIDNEY, EPIDIDYMUS  
 AND TESTIS.  
 CC -1- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.  
 CC  
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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).
CC	-----
DR	EMBL; AF125176; AAD55358.1; -.
DR	HSSP; P02671; 1FZD.
DR	MCD; MG1:1347002; AngptL2.
DR	InterPro; IPR002181; Fibrinogen_C.
DR	Pfam; PF00147; fibrinogen_C; 1.
DR	SMART; SM00186; FBG; 1.
DR	PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
KW	Signal: coiled coil; Glycoprotein.
FT	SIGNAL 1 19
FT	CHAIN 1
FT	CHAIN 20 493
FT	DOMAIN 77 115
FT	DOMAIN 152 202
FT	DOMAIN 438 450
FT	CARBOHYD 164 164
FT	CARBOHYD 192 192
QO	SEQUENCE 493 AA: 57118 MW: 228855ABEF0746BF2 CRC64:
	POTENTIAL.
	ANGIOPLETIN-RELATED PROTEIN 2.
	COILED COIL (POTENTIAL).
	COILED COIL (POTENTIAL).
	FIBRINOGEN C-TERMINAL.
	N-LINKED (GLCNAC. . .) (POTENTIAL).
	N-LINKED (GLCNAC. . .) (POTENTIAL).
	228855ABEF0746BF2 CRC64:

Query Match	20.0%	Score 400.5	DB 1	Length 493
Best Local Similarity	26.7%	Pred. No. 1.1e-24		
Matches 107; Conservative	66;	Mismatches 107;	Indels 121;	Gaps 15;

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OY 48 KTKTIREKHMECNLONLSIYSVRSTKLLRYNMDDQASLDYLSNVQVLENNRYLLT 107
Db 119 EVKLLRKES-----RNNKSRV-----TOLYMLLHETIKRDNAL-----ELSDENRILNCT 166
OY 108 TEVER-----KOLD-----PRPAR----- 122
Db 167 ADMQLASKYKDEHKFOHMLAMLNQSEVLAQLEHCQVRPARPRRPARPRVYQ 226
OY 123 -----VSH-----GLDSTDIKDTIGSYTTPSG----- 146
Db 227 PPTVNRILNOSTNEISDONLKVLPRESLTMPALTSLPSTBPKPSGWRDCLQALEDH 286
OY 147 ----LIIHPEGSYPREVMODMYREGGMVYIOKRIDGILIDPQRLMCVDYLDGFGDLE 202
Db 287 STSYIYLVKPRNTRRLMQVMCDQDHRDGGMTVYIORKIDGSEVNEFRMMETYKQGFGNIDGE 346
OY 203 FWLGLAKTIFYLVNOKNTSFMLUYALESEDOTLVAASYDNWLEDETFKFKMHLGRYSGNA 262
Db 347 YWLELENITYWLTNGN--YKLTVMEDWMSGRKPAEVAASRLPERESYUYLRIQGRHNGNA 404
OY 263 GDAFRGLKEDNONAMPSTSDVNDNDCSRACPLAVNIGOSYKSGHLLHNTGSMWNEEGCLAN 322
Db 405 GDSEFTW-----HNGKOFITLDRDHD-----UYTG--NCAH-YOKGGWVYNACASHN 447
OY 323 LNGIHHFSGLLA---TGIGMGVTKTKNNSPVYKLKYSVMKTR 360
Db 448 LNVGYRGGHYRSTRYODGYVAWE--RGGSYSLKKVVMYMR 486

```

RESULT	5			
ANL2_HUMAN				
ID	ANL2_HUMAN	STANDARD;	PRT;	493 AA.
AC	Q9UK09;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Angioprotein-1-related protein 2 precursor (Angioprotein-like 2).			
GN	ANGPTL2 OR ARP2.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
OX	NCBI_TaxID:9606;			
RN	[1]			
RN	SEQUENCE FROM N.A.			
RP	TISSUE=Heart;			
RC	MEDLINE:99403103; PubMed:10473614;			
RA	Kim I., Moon S.-O., Koh K.N., Kim H., Uhm C.-S., Kwak H.T., Kim N.-G.			

RA Koh G.Y.:  
 RT "Molecular cloning, expression, and characterization of angiotensin-  
 RT related protein. angiotensin-related protein induces endothelial cell  
 RT sprouting.";  
 RL J. Biol. Chem. 274:26523-26528(1999).  
 CC -1- FUNCTION: INDUCES SPROUTING IN ENDOTHELIAL CELLS THROUGH AN  
 CC AUTOCRINE AND PARACRINE ACTION.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED IN HEART, SMALL INTESTINE,  
 CC SPLEEN AND STOMACH. ALSO FOUND IN LOWER LEVELS IN COLON, OVARY,  
 CC ADRENAL GLAND, SKELETAL MUSCLE AND IN PROSTATE.  
 CC -1- PTM: N-GLYCOSYLATED.  
 CC -1- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.  
 CC -----  
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DR	EMBL; AF125175; AAD55357.1; -.	
DR	HSSP; P02671; 1F2D.	
DR	MIM; 605001; -.	
DR	InterPro: IPR002181; Fibrinogen_C.	
DR	Pfam; PF00147; fibrinogen_C; 1.	
DR	SMART; SM00186; FBC; 1.	
DR	ProSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.	
KW	Signal: coiled coil; Glycoprotein.	
FT	SIGNAL	1 22 POTENTIAL.
FT	CHAIN	23 493 ANGIOPOIETIN-RELATED PROTEIN 2.
FT	DOMAIN	76 115 COILED COIL (POTENTIAL).
FT	DOMAIN	152 206 COILED COIL (POTENTIAL).
FT	DOMAIN	438 450 FIBRINOGEN C-TERMINAL.
FT	CARBOHD	164 164 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHD	192 192 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ	SEQUENCE	493 AA; 57104 MM; DF2ADCEB53DI185CA CRC64;

Query Match	20.0%	Score 400;	DB 1;	Length 493;
Best Local Similarity	31.98%	Pred. NO. 1.2e-24;		
Matches 94;	Conservative 50;	Mismatches 93;	Indels 58;	Gaps 11;

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QY 97 NEMNVRVLLTTEVFRKQ-----LDPRRHRVYOSHGLDCTDKDTGYSVTKTSG----- 146
D 211 NRITMQI--STNEIOSODNKLVPRLPRLTMTPLT-----SLPSSYTDKSPGWRDC 278
QY 147 -----LYTIRPESSYSPFEWCMDDYVGGGFWIQRKIDSIIIDFORLACDYLD 194
D 279 LQALEDHGDTSSIYLVAPENRNLQMYWCODGRHDPGSMVLYIQRRLDGSAVAFRNWETYYKQ 338
QY 195 GFQDLLEGFWLGLKRTIYVQKRTSMLYALESDDTLATYASYNFWLEDETRFFKMH 254
D 339 GFGNIDGGYVWGLGENTIYWLNTQGN--KKLLATYMDWSGRVVEAFSAFRLEPSEYYKLR 366
QY 255 LGRYSGNAGDAFRCLKKEDNONAPFSTSDVNDGCRPACLVNGOVSQSCSHLHNTGWM 314
D 397 LGRHGNAGDSFTW-----HNGKQFLTLDRDHD-----VYTG---NCAH-YQKGGWM 439
QY 315 FNEGCLANLNGIHHFSGKLLA---TGLOMGTWIKNNSPVYKISVSKIRRMYPY 366
D 440 YNACAHSLNLCNVWYRGCHYHRSYODGYVAMEF--RGGSYSILKQKVMVIRIRNPPTF 492

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RESULT	6	
FGI1_HUMAN		
ID	STANDARD:	PRT: 312 AA.
AC	O08830; O960M6; O96K66;	
DT	01-MAR-2002 (Rel. 41, Created)	
DT	01-MAR-2002 (Rel. 41, Last sequence update)	
DT	01-MAR-2002 (Rel. 41, Last annotation update)	
DE	Fibrinogen-like protein 1 precursor (hepatocyte-derived fibrinogen)	





Query Match	19.8%	Score 395:	DB 1:	Length 498:
Best Local Similarity	27.0%	Pred. No. 3e-24:		
Matches 116:	Conservative 66:	Mismatches 126:	Indels 122:	Gaps 16

RESULT	9			
AGPL_MOUSE		STANDARD;	PRT;	498 AA.
ID	AGPL_MOUSE			
AC	008538;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Angiopoietin-1 precursor (ANG-1).			
GN	ANGPT1 OR AGPT.			
OS	Mus musculus (Mouse).			
OC	Eumetazoa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheta; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=97134663; PubMed=8980223;			
RA	David S., Aldrich T.H., Jones P.F., Acheson A., Compton D.L., Jain V.,			
RA	Ryan T.E., Bruno J., Radzilewski C., Maissonpierre P.C.,			
RT	Yancopoulos G.D.;			
RT	Isolation of angiopoietin-1, a ligand for the TIE2 receptor, by			

RT	secretion trap expression cloning.";
RL	Cell 87:1161-1169(1996).
CC	-i- FUNCTION: BINDS AND ACTIVATES TIE2 RECEPTOR BY INDUCING ITS
CC	TYROSINE PHOSPHORYLATION. IMPLICATED IN ENDOTHELIAL DEVELOPMENTAL
CC	PROCESSES LATER AND DISTINCT FROM THAT OF VEGF. APPEARS TO PLAY A
CC	CRUCIAL ROLE IN MEDIATING RECIPROCAL INTERACTIONS BETWEEN THE
CC	ENDOTHELIUM AND SURROUNDING MATRIX AND MESENCHYME. MEDIATES BLOOD
CC	VESSEL MATURATION/STABILITY. IT MAY PLAY AN IMPORTANT ROLE IN THE
CC	HEART EARLY DEVELOPMENT.
CC	-i- SUBCELLULAR LOCATION: Secreted.
CC	-i- DEVELOPMENTAL STAGE: EARLY IN DEVELOPMENT, AT E9 TO E11, IT IS
CC	FOUND MOST PROMINENTLY IN THE HEART MYOCARDIUM SURROUNDING THE
CC	ENDOCARDIUM. LATER, IT BECOMES MORE WIDELY DISTRIBUTED, MOST OFTEN
CC	IN THE MESENCHYME SURROUNDING DEVELOPING VESSELS, IN CLOSE
CC	ASSOCIATION WITH ENDOTHELIAL CELLS.
CC	-i- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.
CC	-----
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CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC	or send an email to <a href="mailto:license@isb-slb.ch">license@isb-slb.ch</a> ).
CC	-----
DR	EMBL; U83509; AAB50558.1; .
DR	HSSP; P02671; 1FZD.
DR	MCD; MGI:108448; Aspt.
DR	InterPro; IPR002181; Fibrinogen_C.
DR	Pfam; PF00147; fibrinogen_C; 1.
DR	SMART; SM00186; FBG; 1
DR	PROSITE; PS00514; FTBRIN_AG_C_DOMAIN; 1.
KW	Glycoprotein; Coiled coil; Signal.
FT	SIGNAL
FT	1
FT	19
FT	POTENTIAL.
FT	CHAIN
FT	20
FT	498
FT	ANGIOPOTENTIN-1.
FT	DOMAIN
FT	81
FT	119
FT	COILED COIL (POTENTIAL).
FT	DOMAIN
FT	153
FT	261
FT	COILED COIL (POTENTIAL).
FT	DOMAIN
FT	284
FT	498
FT	FIBRINOGEN C-TERMINAL.
FT	CARBOHD
FT	92
FT	92
FT	N-LINKED (GLCNAC. . . ) (POTENTIAL).
FT	CARBOHD
FT	122
FT	122
FT	N-LINKED (GLCNAC. . . ) (POTENTIAL).
FT	CARBOHD
FT	154
FT	154
FT	N-LINKED (GLCNAC. . . ) (POTENTIAL).
FT	CARBOHD
FT	243
FT	243
FT	N-LINKED (GLCNAC. . . ) (POTENTIAL).
FT	CARBOHD
FT	295
FT	295
FT	N-LINKED (GLCNAC. . . ) (POTENTIAL).
FT	CARBOHD
FT	498
FT	57505 MW; 285B4DDEC260D800 CRC64;
SEQ	SEQUENCE

Query Match	19.6%	Score 391	DB 1	Length 498
Best Local Similarity	26.7%	Pred. No. 6.3e-24		
Matches 115	Conservative	67	Mismatches 126	Indels 122
				Gaps 16
QY	3	VQGNCVHHSDDSSVNVIVEDGSNADKESKNDTYCKEPCDEECSDVKTITREKHFHRCRN	62	
Db	115	IQGNVAVNIT-----ATMLEIGTSLSQ-----AEQTRKLTIVETQVLYNQTSLSEQL	163	
QY	63	LQNSIVSY-----TRSTKRLRNRM	82	
Db	164	LENSLSTYKLEKQLQQTNEILKIHKNLSLEBKILLEMGRHKEELDTLKEKENILGHV	223	
QY	83	DEQQAQLDLYSNQV-----ELM-----NRLLLTTEVF-----RKQDPF	118	
Db	224	SRQTEILQLEKQLSRATNNNSILQKQLELMDTVHNLVLSLCTKGVLLKGGKREERPF	283	
QY	119	PHRPVQSHGLDCTDKDTIGSVTKPRSGLYIIHPGSSYPFEVQMDMDYRGSGGVVIQKR	178	
Db	284	-----RDADVY-----QAGFNKSGIYTTIYFNMPKKVYFCMDVYNGGGMVYIQHR	330	
QY	179	IDGIIDFORLWCMDYLDGFGDLGIEFWLLGSLKTFIYVNOKNTSPMLVYALASEDDTLAYAS	238	
Db	331	EDGSLDPOFGMKMEYKMGFENPSGSEYWLGNELFFAITSQR--GYMLRIELMDQGRNVSQ	388	
QY	239	YQNFMLEDETREFFKMHLGRTSGNAGDAFGLKKEDN--QNAFPSTISVDYNDGCRAPC--	294	
Db	389	YQRFHIGNKQVRYLTKLKHGTAG-----KQSSLLHGADFSTKPADNDNCMKCAL	441	

OY 295 LVNGSVKSCSLHNKTMWNECCGLANGLNHHSS-----GKLLATGICMGWTNKNNSPV 350  
DB 442 MULTG-----GWMFDCGSPNLNGMFTYAGQNHGKL--NGIKWHYF--KGPSY 484  
OY 351 KIKSVSMKIR 360  
DB 485 SURSTTMIR 494  
RESULT 10  
AGP2\_HUMAN  
ID AGP2\_HUMAN STANDARD: PRT: 496 AA.  
AC 015123: Q9NRR7;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Angiopoietin-2 precursor (ANG-2).  
GN ANGPT2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RC SEQUENCE FROM N.A. (ISOFORM 1).  
RX TISSUE=Lung;  
RA MEDLINE=97349327; PubMed=9204896;  
RA Madsompiere P.C., Suri C., Jones P.F., Bartunkova S., Wiegand S.J.,  
RA Radziejewski C., Compton D., McClain J., Aldrich T.H.,  
RA Papadopoulos N., Daly T.J., Davis S., Sato T.N., Yancopoulos G.D.,  
RA "Angiopoietin-2, a natural antagonist for tie2 that disrupts in vivo  
RT angiogenesis.";  
RL Science 277:55-60(1997).  
RN [2]  
RN SEQUENCE FROM N.A. (ISOFORM 2).  
RC TISSUE=umbilical vein endothelial cells;  
RX MEDLINE=20309815; PubMed=10766762;  
RA Kim I., Kim J.-H., Ryu Y.S., Jung S.H., Nah J.J., Koh G.Y.,  
RT "Characterization and expression of a novel alternatively spliced  
RT human angiopoietin-2.";  
RL J. Biol. Chem. 275:18550-18556(2000).  
CC -1- FUNCTION: BINDS TO TIE2 RECEPTOR AND COUNTERACTS BLOOD VESSEL  
CC MATURATION/STABILITY MEDIATED BY ANGIOPOIETIN-1. ITS FUNCTION MAY  
CC BE CONTEXT-DEPENDENT. IN THE ABSENCE OF ANGIOGENIC INDUCERS, SUCH  
CC AS VEGF, ANG2-MEDIATED LOOSENING OF CELL-MATRIX CONTACTS MAY  
CC INDUCE ENDOTHELIAL CELL APOPTOSIS WITH CONSEQUENT VASCULAR  
CC REGRESSION. IN CONCERT WITH VEGF, IT MAY FACILITATE ENDOTHELIAL  
CC CELL MIGRATION AND PROLIFERATION, THUS SERVING AS A PERMISSIVE  
CC ANGIOGENIC SIGNAL.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are  
CC produced by alternative splicing.  
CC -1- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.  
CC -----  
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CC -----  
DR EMBL: AF004327; AAB63190.1; -  
DR EMBL: AF187858; AAF76526.1; -  
DR HSSP: P02671; 1FZD.  
DR MIM: 601922; -  
DR InterPro: IPR002181; Fibrinogen\_C.  
DR Pfam: PF00147; Fibrinogen\_C; 1.  
DR SMART: SM00186; FBG; 1.  
DR PROSITE: PS00514; FIBRIN-AG-C-DOMAIN; 1.  
KW Glycoprotein; Coiled coil; Signal; Alternative splicing.  
FT SIGNAL 1 16  
FT CHAIN 17 496 ANGIOPOIETIN-2.

FT DOMAIN 130 256 COILED COIL (POTENTIAL).  
FT 280 496 FIBRINOGEN C-TERMINAL.  
FT CARBOHYD 89 89 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 119 119 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 133 133 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 240 240 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 304 304 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT VARSPLIC 97 148 MISSING (IN ISOFORM 2).  
SQ SEQUENCE 496 AA; 56919 MW; 5642A58847A7385C CRC64;  
Query Match 19.1%; Score 381.5; DB 1; Length 496;  
Best Local Similarity 26.3%; Pred. No. 3.6e-23;  
Matches 110; Conservative 73; Mismatches 138; Indels 97; Gaps 16;  
OY 3 VQNCVHHSTDSVYNAIVVDGNSNADDESNTVCKEDEDSCDVYTKI-----TREE--- 55  
DB 112 IQQNAVQNOT---AVMIDIGTLNLTQ-----AEQTRKLTDEAQLNQTTRLEQL 160  
OY 56 -RHFMCRN-LQNSIYSYTRSTFKL-----LRNMDEQOASL 89  
DB 161 LEHSLSTNKLKQLIDQTEIKKLDQKNSFLKKVYAMEDKHIIQLQSIKEKQDLQVLY 220  
OY 90 DYLSNOVNELMNRVLLT--TEVFRKQ-----LDPRHAPVOSH 126  
DB 221 SKQNSIIELEKRIYATVYNNVSLQKQHDLMETVNNLTMTASTNSAKDPYVAREQIS 280  
OY 127 GIDCTDIXKTISVYKTPSPGLYIIHPEGSSYFEVWCMDYRGCGTGYOKRIDIDPQ 186  
DB 281 FPDCAEVFKS-----GHTTGITLTLPNSTEIRKAYCDWAGGWTIIQREDDSVDPQ 336  
OY 187 RLWCYLDGFGDLDGEFWLGLKRIFYVQKNTSFMLYVALESDDTLVASYDNFMFL 246  
DB 337 RHWKEKYVGEFNPSPGEYTWLGNFVSQLTNQQR--VYLKHLKLDWGENEYSLXEHYLS 394  
OY 247 ETRFFKMLHGRYSGNAGDAFRGLKEDNONAMPFSTSDVNDGCRPACLVNGSVKSCSH 306  
DB 395 EELNVRHILHKLGLTGTAQKI-----SSISQPGNDFSTKDGDNKDC-----ICKSQ 439  
OY 307 LVNGKGMWNECCGLANGLNHH-----FSGKLLATGICMGWTNKNNSPVKIKSVSMKIR 360  
DB 440 MLT-GGMWFDACGSPNLNGMFTYAGQNHGKL--NGIKWHYF--KGSYSLAKATTMIR 492  
RESULT 11  
FIBB\_HUMAN  
ID FIBB\_HUMAN STANDARD: PRT: 491 AA.  
AC P02675;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 01-JUL-1993 (Rel. 26, Last sequence update)  
DT 01-MAR-2002 (Rel. 41, Last annotation update)  
DE Fibrinogen beta chain precursor [Contains: Fibrinopeptide B].  
GN FGB.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RN SEQUENCE FROM N.A.  
RX MEDLINE=91344740; PubMed=2102623;  
RA Chung D.W., Harris J.E., Davie E.W.,  
RT "Nucleotide sequences of the three genes coding for human  
RT fibrinogen.";  
RL Adv. Exp. Med. Biol. 281:39-48(1990).  
RN [2]  
RN SEQUENCE FROM N.A.  
RX MEDLINE=83283433; PubMed=6688356;  
RA Chung D.W., Que B.G., Rixon M.W., Mace M. Jr., Davie E.W.,  
RT "Characterization of complementary deoxyribonucleic acid and genomic  
RT deoxyribonucleic acid for the beta chain of human fibrinogen.";  
RL Biochemistry 22:3244-3250(1983).  
RN [3]

RP SEQUENCE FROM N.A.  
 RA Chung D.W., Harris J.E., Davie E.W.;  
 RT "Nucleotide sequences of the three genes coding for human  
 fibrinogen.";  
 RL (in) Liu C.Y., Chien S. (eds.);  
 RL fibrinogen, thrombosis, coagulation and fibrinolysis, pp.39-48,  
 RL Plenum Press, New York (1991).  
 RN [4]  
 RP SEQUENCE OF 31-491, AND CARBOHYDRATE-LINKAGE SITE.  
 RA Henschen A., Lottspeich F., Southan C., Topfer-Petersen E.;  
 RT "Human fibrinogen: sequence, sulfur bridges, glycosylation and some  
 structural variants.";  
 RL (in) Peeters H. (eds.);  
 RL Provides of the biological fluids, Proc. 28th colloquium, pp.51-56,  
 RL Pergamon Press, Oxford (1980).  
 RN [5]  
 RP SEQUENCE OF 31-491.  
 RX MEDLINE-79124640; PubMed-420779;  
 RA Watt K.W.K., Takagi T., Doolittle R.F.;  
 RT "Amino acid sequence of the beta chain of human fibrinogen.";  
 RL Biochemistry 18:68-76(1979).  
 RN [6]  
 RP SEQUENCE OF 31-148, AND DISULFIDE BONDS.  
 RX MEDLINE-76225080; PubMed-936108;  
 RA Blomback B., Hessel B., Hogg D.;  
 RT "Disulfide bridges in NH2-terminal part of human fibrinogen.";  
 RL Thromb. Res. 8:639-658(1976).  
 RN [7]  
 RP SEQUENCE OF 1-38 FROM N.A.  
 RX MEDLINE-87146483; PubMed-3029722;  
 RA Huber P., Dalmon J., Courtois G., Laurent M., Assouline Z.,  
 RA Marguerie G.;  
 RT "Characterization of the 5'-flanking region for the human fibrinogen  
 beta gene.";  
 RL Nucleic Acids Res. 15:1615-1625(1987).  
 RN [8]  
 RP SEQUENCE OF 31-44.  
 RA Blomback B., Blomback M., Grondahl N.J., Guthrie C., Hinton M.;  
 RT "Studies on fibrinopeptides from primates.";  
 RL Acta Chem. Scand. 19:1788-1789(1965).  
 RN [9]  
 RP REVIEW, AND DISULFIDE BONDS.  
 RX MEDLINE-83254370; PubMed-6575689;  
 RA Henschen A., Lottspeich F., Kehl M., Southan C.;  
 RT "Covalent structure of fibrinogen.";  
 RL Ann. N.Y. Acad. Sci. 408:28-43(1983).  
 RN [10]  
 RP DISULFIDE BONDS.  
 RX MEDLINE-77245999; PubMed-891553;  
 RA Gaarlund B., Hessel B., Marguerie G., Murano G., Blomback B.;  
 RT "Primary structure of human fibrinogen. Characterization of  
 disulfide-containing cyanogen-bromide fragments.";  
 RL Eur. J. Biochem. 77:595-610(1977).  
 RN [11]  
 RP DISULFIDE BONDS.  
 RA Doolittle R.F., Takagi T., Watt K.W.K., Bouma H. III, Cottrell B.A.,  
 RA Cassman K.G., Goldbaum D.M., Doolittle L.R., Friesner S.J.;  
 RT "The structures of fibrinogen and fibrin.";  
 RL (in) Magnusson S., Ottesen M., Foltmann B., Dano K.,  
 RL Neurath H. (eds.);  
 RL Regulatory proteolytic enzymes and their inhibitors, pp.163-172,  
 RL Pergamon Press, New York (1978).  
 RN [12]  
 RP REVIEW, EM STRUCTURE, POLYMERIZATION, AND LIGANDS.  
 RX MEDLINE-84305751; PubMed-6383194;  
 RA Doolittle R.F.;  
 RT "Fibrinogen and fibrin.";  
 RL Annu. Rev. Biochem. 53:195-229(1984).  
 RN [13]  
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 164-491.  
 RX MEDLINE-97472408; PubMed-9333233;  
 RA Spraggon G., Everse S.J., Doolittle R.F.;  
 RT "Crystal structures of fragment D from human fibrinogen and its

RT crosslinked counterpart from fibrin.";  
 RL Nature 389:455-462(1997).  
 RN [14]  
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 164-491.  
 RX MEDLINE-98292395; PubMed-9628725;  
 RA Everse S.J., Spraggon G., Veerapandian L., Riley M., Doolittle R.F.;  
 RT "Crystal structure of fragment double-D from human fibrin with two  
 RT different bound ligands.";  
 RL Biochemistry 37:8637-8642(1998).  
 RN [15]  
 RP X-RAY CRYSTALLOGRAPHY.  
 RX MEDLINE-99175089; PubMed-10074346;  
 RA Everse S.J., Spraggon G., Veerapandian L., Doolittle R.F.;  
 RT "Conformational changes in fragments D and double-D from human  
 fibrin(ogen) upon binding the peptide ligand Gly-His-Arg-Pro-amide.";  
 RL Biochemistry 38:2941-2946(1999).  
 RN [16]  
 RP VARIANT BALTIMORE-2.  
 RX MEDLINE-89058942; PubMed-3194892;  
 RA Schmelzer C.H., Ebert R.F., Bell M.R.;  
 RT "A polymorphism at B beta 448 of fibrinogen identified during  
 RT structural studies of fibrinogen Baltimore II.";  
 RL Thromb. Res. 52:173-177(1988).  
 RN [17]  
 RP VARIANT ISE.  
 RX MEDLINE-91208409; PubMed-2018836;  
 RA Yoshida N., Wada H., Morita K., Hirata H., Matsuda M., Yamazumi K.,  
 RA Asakura S., Shirakawa S.;  
 RT "A new congenital abnormal fibrinogen Ise characterized by the  
 RT replacement of B beta glycine-15 by cysteine.";  
 RL Blood 77:1958-1963(1991).  
 RN [18]  
 RP VARIANT NAPLES.  
 RX MEDLINE-92340664; PubMed-1634610;  
 RA Koopman J., Haverkate F., Lord S.T., Grimbergen J., Mannucci P.M.;  
 RT "Molecular basis of fibrinogen Naples associated with defective  
 RT thrombin binding and thrombophilia. Homozygous substitution of B beta  
 RT 68 Ala->Thr.";  
 RL J. Clin. Invest. 90:238-244(1992).  
 RN [19]  
 RP VARIANTS JUMIDEN AND NIMEGEN.  
 RX MEDLINE-92228809; PubMed-1565641;  
 RA Koopman J., Haverkate F., Grimbergen J., Engesser L., Novakova I.,  
 RA Kerst A.F.J.A., Lord S.T.;  
 RT "Abnormal fibrinogens Jumiden (B beta Arg14->Cys) and Nijmegen (B  
 RT beta Arg44->Cys) form disulfide-linked fibrinogen-albumin  
 RT complexes.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:3478-3482(1992).  
 RN [20]  
 RP VARIANT NEW YORK-1.  
 RX MEDLINE-85157605; PubMed-3156856;  
 RA Liu C.Y., Koehn J.A., Morgan F.J.;  
 RT "Characterization of fibrinogen New York 1. A dysfunctional  
 RT fibrinogen with a deletion of B beta(9-72) corresponding exactly to  
 RT exon 2 of the gene.";  
 RL J. Biol. Chem. 260:4390-4396(1985).  
 CC -I- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT  
 CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET  
 CC AGGREGATION.  
 CC -I- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS  
 CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.  
 CC THE AMINO ENDS OF ALL CHAINS ARE CONTAINED IN THE CENTRAL NODULE.  
 CC DIVERGING FROM THIS NODULE ARE 2 THREE-CHAIN COILED COILS, WHICH  
 CC CONNECT THE CENTRAL NODULE TO THE DISTAL NODULES CONTAINING THE  
 CC DISTAL DOMAINS. EXTENDING FAR PERIPHERALLY ARE THE LONG CARBOXYL  
 CC ENDS OF THE ALPHA CHAINS.  
 CC -I- DISEASE: DEFECTS IN FGB ARE A CAUSE OF THROMBOPHILIA.  
 CC -I- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY  
 CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA  
 CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES  
 CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT. THE SOFT CLOT IS  
 CC CONVERTED INTO THE HARD CLOT BY FACTOR XIII WHICH CATALYZES THE  
 CC EPSILON-(GAMMA-GLUTAMYL)LYSINE CROSS-LINKING BETWEEN GAMMA CHAINS



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CC (STRONGER) AND BETWEEN ALPHA CHAINS (WEAKER) OF DIFFERENT
CC MONOMERS.
CC -I- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: J00129; AAA52429.1; -
DR EMBL: J00131; AAA98115.1; -
DR EMBL: J00130; AAA98115.1; JOINED.
DR EMBL: J00132; AAA98116.1; -
DR EMBL: J00133; -; NOT_ANNOTATED_CDS.
DR EMBL: X05018; CAA28674.1; -
DR EMBL: M64983; AAA18024.2; -
DR EMBL: M26877; AAA52445.1; -
DR PIR: B43568; FGHUB.
DR PDB: 1FZA; 03-DEC-97.
DR PDB: 1FZB; 03-DEC-97.
DR PDB: 1FZC; 14-OCT-98.
DR PDB: 1FZE; 08-JUN-99.
DR PDB: 1FZF; 08-JUN-99.
DR PDB: 1FZG; 08-JUN-99.

Query Match 18.8%; Score 375.5; DB 1; Length 491;
Best Local Similarity 26.6%; Pred. No. 1.1e-22;
Matches 118; Conservative 56; Mismatches 142; Indels 127; Gaps 17;

QY 5 GNCVHSTSDSVNIVEDGNSNAKDESKSNDTVCKEDCESCVKTKRTREKHFCRMQD 64
Db 93 GGCILHADBDGLV-----CPGCOLDEALLQDE-----RPIR 124
QY 65 NSI-----VYTRSTK-----KLRLNMDQASLDYLSNOVELMN----- 101
Db 125 NSVDELNNVNAVSTSSSFQYMYLLKDLQKQKQKQKQKQKQKQKQKQKQKQKQKQK 184
QY 102 -----RVLLTTEVFRRKQDPP-----HRYQSHGLDCTD 132
Db 185 ETVNSNITPNLRVLSILENLRKIQKLESDVSAOMEYCRTPTCYSCNIPVVS-CKECE 243
QY 133 IKDTIGSVTKTPSGLYIHPGSSYPFEVCMDDYRGSGWTYQKRIQIDIDFORLQNDY 192
Db 244 IIRKGET-----SEMYLLQPDSSVPRVYVCDMTENGWTVIQNRQDSVDFGRKMDPY 299
QY 193 LDGFD-----LGEFWLGLKIPYIVQKNTSFLYALLESDDTLAYSTD 240
Db 300 KQGFENVATNTDGKNYGLPGEYWLGNDKISQLTRMGPE--LLIEMDMKDKVKAHNG 357
QY 241 NFWLEDETRFPMHLGRYSNAGDAFRG-----LKKEDN-----QNPAPSTSDVNDGCRP 292
Db 358 GETVQNEANKKQVSVNKRGRAGNLMGASQLMGENRMTHTHNGMFTSYRDNDG--- 414
QY 293 ACLVNGQSVKCSHLNKTGMWNEGCLANLNGIHFSKLT-----LATGIQMGWTWT 344
Db 415 --WLTSIDPRKQCS-EDGSGMWYNRCHAAHPGRYMGQYTWDAKAGTDDGVVMMNN- 470
QY 345 KNSPVKIKSVSMKTRKMYNPYF 367
Db 471 -KGSWYSMRKSMKTR---PFF 488

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DE Angiopoietin-2 (ANG-2) (Fragment).
GN ANGPT2 OR ANG2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID:9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE:Ovary;
RA Medline:99054348; PubMed:9840613;
RT Goede V., Schmidt T., Krimina S., Kozian D., Augustin H.G.;
RT "Analysis of blood vessel maturation processes during cyclic ovarian
RT lab. Invest. 78:1385-1394(1998).
RN [2]
RP SEQUENCE OF 219-355 FROM N.A.
RC TISSUE:Adrenal cortex;
RA Medline:98451564; PubMed:9776732;
RT Mandriola S.J., Pepper M.S.;
RT "Regulation of angiopoietin-2 mRNA levels in bovine microvascular
RT endothelial cells by cytokines and hypoxia.";
RL Circ. Res. 83:852-859(1998).
CC -I- FUNCTION: BINDS TO TIE2 RECEPTOR AND COUNTERACTS BLOOD VESSEL
CC MATURATION/STABILITY MEDIATED BY ANGIOPOIETIN-1. ITS FUNCTION MAY
CC BE CONTEXT-DEPENDENT. IN THE ABSENCE OF ANGIOGENIC INDUCERS, SUCH
CC AS VEGF, ANG2-MEDIATED LOOSENING OF CELL-MATRIX CONTACTS MAY
CC INDUCE ENDOTHELIAL CELL APOPTOSIS WITH CONSEQUENT VASCULAR
CC REGRESSION. IN CONCERT WITH VEGF, IT MAY FACILITATE ENDOTHELIAL
CC CELL MIGRATION AND PROLIFERATION, THUS SERVING AS A PERMISSIVE
CC ANGIOGENIC SIGNAL.
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- DEVELOPMENTAL STAGE: FOUND TO BE EXPRESSED THROUGHOUT THE OVARIAN
CC CYCLE. OVEREXPRESSED DURING LUTEOLYSIS, THIS COULD REFLECT THE
CC REGRESSION OF CAPILLARIES THAT HAD DEVELOPED PERICYTE CONTACT IN
CC THE MIDSTAGE CORPUS LUTEUM.
CC -I- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.
CC -----
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CC -----
DR EMBL: AF094699; AAC62490.1; -
DR EMBL: AF032924; AAC78285.1; -
DR HSSP: P02671; 1FZD.
DR InterPro: IPR002181; Fibrinogen_C.
DR Pfam: PF00147; Fibrinogen_C.1.
DR SMART: SM00186; FBG.1.
DR PROSITE: PS00514; FIBRIN_AG_C_DOMAIN; 1.
KW Glycoprotein; Coiled coil.
FT DOMAIN 1 138 COILED COIL (POTENTIAL).
FT DOMAIN 139 375 FIBRINOGEN C-TERMINAL.
FT CARBOHYD 13 13 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 31 31 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 120 120 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 272 272 S->L (IN REF. 2).
SQ SEQUENCE 375 AA; 42761 MW; 6F086C4A5C80050A CRC64;

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Query Match 18.8%; Score 375; DB 1; Length 375;
Best Local Similarity 30.2%; Pred. No. 8.4e-23;
Matches 112; Conservative 57; Mismatches 136; Indels 66; Gaps 15;

QY 11 STDSSVNVIVEDGNSNAKDESKSNDTVCKE--DCEESCVKTKRTREKHFM--CNLQNS 66
Db 46 STNKLKQILDTQTSISKLQDKNSFLKKYLDMEKHIVQLRSIKERDQGLVAVSKQNS 105

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QY 67 IVSYTRS---TKLLRNMDQOASLDYLSNOVELMNR-----VLLTTE--VERKOLD 116
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 106 IIELEKQLVATAYNNNSVLOKQOHDLMETVNNLTLMSTSPSLAKDEQIIFR---- 161
QY 117 PEPHAPVSHGLDCTDIKDTIGSVTK--TPSGLYIIHPEGSSYPFEVCMDDYRGSGWT 173
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 162 -----DC-----GEAFKSGLTFTSGVYTLTFPSTPEIRKAYCDMETGGGWT 202
QY 174 VIOKRIDGIIIDFORLMDYLDGFGDLGEPWLGAKIIFYVONKNTSPMLVALESEDDT 233
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 203 VIOKREGSDVDFORTWKEKYKGFENPSEHMLGNEFVSQVYGOGR--YVLKIHLDMEGN 260
QY 234 LAVASYNFMLEDETRFFKMHILGRYSNAGDAFRGLKEDNOMAMPSTSDVNDGCRPA 293
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 261 EASLYIHFIYSNELNRIHLKGLTGTAKEI-----SSISQPNDSFTKDADNDKC--- 312
QY 294 CLVNGOSVKSCHLHNTKGMWFNECGLANLNGIH---FSGKLLATGIQWGTWTKNNSP 349
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 313 -----ICKSQMLT-GGWMFDCGSPSNLNGMYYPORQNTNKF--NGIKWYV--KGS 360
QY 350 VKIKSVSMKIR 360
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 361 YSLKATTMIR 371

RESULT 13
AGP2_MOUSE
ID AGP2_MOUSE STANDARD: PRT: 496 AA.
AC 035608;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Angiopoietin-2 precursor (ANG-2).
GN ANGPT2 OR AGPT2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RX MEDLINE=97349327; PubMed=9204896;
RA Misoplarre P.C., Suri C., Jones P.F., Bartunkova S., Wiegand S.J.,
RA Radzilewski C., Compston D.L., McClain J., Aldrich T.H.,
RA Papadopoulos N., Daly T.J., Davis S., Sato T.N., Yancopoulos G.D.;
RT "Angiopoietin-2, a natural antagonist for Tie2 that disrupts in vivo
RT angiogenesis.";
RL Science 277:55-60(1997).
CC -1- FUNCTION: BINDS TO TIE2 RECEPTOR AND COUNTERACTS BLOOD VESSEL
CC MATURATION/STABILITY MEDIATED BY ANGIOPOIETIN-1. ITS FUNCTION MAY
CC BE CONTEXT-DEPENDENT. IN THE ABSENCE OF ANGIOGENIC INDUCERS, SUCH
CC AS VEGF, ANG2-MEDIATED LOOSENING OF CELL-MATRIX CONTACTS MAY
CC INDUCE ENDOTHELIAL CELL APOPTOSIS WITH CONSEQUENT VASCULAR
CC REGRESSION. IN CONCERT WITH VEGF, IT MAY FACILITATE ENDOTHELIAL
CC CELL MIGRATION AND PROLIFERATION, THUS SERVING AS A PERMISSIVE
CC ANGIOGENIC SIGNAL.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: EXPRESSED ONLY AT SITES OF VASCULAR
CC REMODELING.
CC -1- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.
CC -----
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CC -----
CC EMBL: AF004326; AAB63189.1; -.
CC HSSP: P02671; IFTD.
CC MGD: MGI:1202890; Agp2.
CC InterPro: IPR002181; Fibrinogen_C.

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DR Pfam: PF00147; fibrinogen_C. 1.
DR SMART: SM00186; FBG: 1.
DR PROSITE: PS00514; FIBRIN_AG_C-DOMAIN; 1.
KW Glycoprotein; Coiled coil; Signal.
FT SIGNAL 1 18
FT CHAIN 19 496
FT DOMAIN 159 256
FT DOMAIN 280 496
FT CARBOHYD 89 89
FT CARBOHYD 119 119
FT CARBOHYD 133 133
FT CARBOHYD 151 151
FT CARBOHYD 240 240
FT CARBOHYD 304 304
SQ SEQUENCE 496 AA; 56616 MW; FA3021FE4ED1C410 CRC64;

Query Match 18.7%; Score 374.5; DB 1; Length 496;
Best Local Similarity 25.5%; Pred. No. 1,3e-22;
Matches 110; Conservative 72; Mismatches 125; Indels 125; Gaps 16;

QY 3 VQNCVHHSSTDSVYNIVEDGSKNAKDESKSNDYCKEDCECDYKRTIREKHFCRN 62
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 112 IQQWVVOQT---AVMIEIGTSLNQTA-----QTRKLTDEVAQVLTQTRLEQL 160
QY 63 LQNSIVSTRSTKLLNNMDQOASLDYLSNOVELMNRVLLTTEVF----- 111
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 161 LQHSI-----STNKLKQILDO-----TSEINKLQNKSFLEQVLDMEGRHSEQL 207
QY 112 -----RKQ---LDPPFHPV-----QSHGIDCYDIDKDTIGSVTK-- 142
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 208 SMKQKQELQVLSKQSSVIDELEKILVATVNNSLQKQH-----DLMETVNSLTMM 262
QY 143 -----TPSGLYIIHPEGSSYPFEVCMDDYRGSGW 172
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 263 SSPSKSSVAIRKEQTTFRDCAEIFKSGLTTSGLTFTFPNSTPEIRKAYCDMDYGGGW 322
QY 173 TVIOKRIDGIIIDFORLMDYLDGFGDLGEPWLGAKIIFYVONKNTSPMLVALESEDD 232
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 323 TVIOHREDGSDVDFORTWKEKYKGFENPSEHMLGNEFVSQVYGOGR--YVLKIQLKMEG 380
QY 233 TLAVASYDNFMLEDETRFFKMHILGRYSNAGDAFRGLKEDNOMAMPSTSDVNDGCRP 292
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 381 NEASLIDHFIYLAAGEESVRIHLTGITGTAKEI-----SSISQSGSPSTKDSNDKC-- 433
QY 293 ACLVNGOSVKSCHLHNTKGMWFNECGLANLNGIH---FSGKLLATGIQWGTWTKNNS 348
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 434 -----ICKSQMLT-GGWMFDCGSPSNLNGQYYPQKQNTNKF--NGIKWYV--KGS 480
QY 349 PVKIKSVSMKIR 360
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 481 GYSLKATTMIR 492

RESULT 14
FIBR_RAT
ID FIBR_RAT STANDARD: PRT: 479 AA.
AC P14480;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Fibrinogen beta chain precursor [Contains: Fibrinopeptide B].
GN FGB.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Liver;
RX MEDLINE=95143386; PubMed=7841303;
RA Courtney M.A., Buncie L.A., Neroni L.A., Simpson-Haidaris P.J.;
RT "Cloning of the complete coding sequence of rat fibrinogen B beta

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RT chain cDNA: interspecies conservation of fibrin beta 15-42 primary  
 RT structure.";  
 RL Blood Coagul. Fibrinolysis 5:487-496(1994).  
 RN [2]  
 RP SEQUENCE OF 1-26 FROM N.A.  
 RX MEDLINE=84194000; Pubmed=6232608;  
 RT Fowlkes D.M., Mullis N.T., Comeau C.M., Crabtree G.R.:  
 "Potential basis for regulation of the coordinately expressed  
 fibrinogen genes: homology in the 5' flanking regions.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 81:2313-2316(1984).  
 RN [3]  
 RP SEQUENCE OF 19-32.  
 RA Blomback B., Blomback M., Grondahl N.J.:  
 "Studies on fibrinopeptides from mammals.";  
 RL Acta Chem. Scand. 19:1789-1791(1965).  
 RN [4]  
 RP SEQUENCE OF 183-479 FROM N.A.  
 RX MEDLINE=89378771; Pubmed=2673932;  
 RA Eastman E.M., Giulia N.B.:  
 "Cloning and characterization of a cDNA for the B beta chain of rat  
 fibrinogen: evolutionary conservation of translated and  
 3'-untranslated sequences.";  
 RT Gene 79:151-158(1989).  
 RN [5]  
 RP SEQUENCE OF 425-479 FROM N.A.  
 RC STRAIN-WISTAR; TISSUE=Liver;  
 RX MEDLINE=87134033; Pubmed=3817019;  
 RA Sobczak J., Lotli A.-M., Taroux P., Duguet M.:  
 "Molecular cloning of mRNA sequences transiently induced during rat  
 liver regeneration.";  
 RT Exp. Cell Res. 169:47-56(1987).  
 CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT  
 CC -1- POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET  
 CC AGGREGATION.  
 CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS  
 CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.  
 CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY  
 CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA  
 CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES  
 CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.  
 CC -1- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.  
 CC -----  
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 CC -----  
 DR EMBL; U05675; AAA64866.1; -;  
 DR EMBL; M27220; AAA41160.1; -;  
 DR EMBL; K01336; AAA98625.1; -;  
 DR EMBL; M35602; AAA41159.1; -;  
 DR PIR; A05299; A05299.  
 DR PIR; PE0010; PE0010.  
 DR HSSP; P02673; 1FZE.  
 DR InterPro; IPR002181; Fibrinogen\_C.  
 DR Pfam; PF00147; fibrinogen\_C; 1.  
 DR SMART; SM00186; FBG; 1.  
 DR PROSITE; PS00514; FIBRIN\_AG\_C\_DOMAIN; 1.  
 KM Blood coagulation; Plasma; Glycoprotein; Signal.  
 DR SIGNAL 1 18  
 FT CHAIN 19 479 FIBRINOGEN BETA CHAIN.  
 FT PEPTIDE 19 32 FIBRINOPEPTIDE B.  
 FT DISULFID 211 211 INTERCHAIN (WITH THE ALPHA CHAIN)  
 FT (BY SIMILARITY).  
 FT DISULFID 215 215 INTERCHAIN (WITH THE GAMMA CHAIN)  
 FT (BY SIMILARITY).  
 FT DISULFID 219 304 (BY SIMILARITY).  
 FT DISULFID 229 258 BY SIMILARITY.  
 FT DISULFID 412 425 BY SIMILARITY.  
 FT CARBOHYD 382 382 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CONFLICT 28 30 LSI -> ILS (IN REF. 3).  
 FT CONFLICT 439 439 L -> Q (IN REF. 5).  
 FT CONFLICT 441 441 S -> T (IN REF. 5).  
 FT CONFLICT 445 445 S -> A (IN REF. 5).  
 FT CONFLICT 467 467 R -> K (IN REF. 5).  
 FT CONFLICT 475 475 V -> F (IN REF. 5).  
 SQ SEQUENCE 479 AA; 54303 MW; EC6C6B77C3E0EC0 CAC64;  
 Query Match 18.7%; Score 373.5; DB 1; Length 479;  
 Best Local Similarity 27.2%; Pred. No. 1.5e-22;  
 Matches 119; Conservative 49; Mismatches 149; Indels 121; Gaps 15;  
 QY 5 GNCVHSTDSVYNIVEDGSNAKDSKSDIYCKEDCESCVKRTITREEHFPCRLQ 64  
 DB 81 GGCYHDDGDMGL-----CATGCELRDTLLNHE-----RPik 112  
 QY 65 NSIV-----SYTRSTKTLRRMDEQASLDIYSNONE----- 98  
 DB 113 NSIAELNSINSVYETSSVTFQYLTLLDKMVKKQKQAVKDNENVINEYSSILEDKLYID 172  
 QY 99 -----LMNRVLLLTVEFRKOLD-----PEFHRPQSH-----GLDCTDI 133  
 DB 173 ETVNDNIPRLNLRSLIEDLRSMQKLESDISAQTEYCHPTVCYNIPVYSGKECEBI 232  
 QY 134 KPTIGSVKTPSGLYIHPESSYPEEWCMDYRGCGFTVYQKRIIDGIDFQRLMCDYL 193  
 DB 233 IRKGCEFT-----SEMYLIQPDTSKPRVYCDKMTENGSGWTYIONODGSVDFGRKMDPYK 288  
 QY 194 DGFGE-----LIGFEPLGLKRTFYVNGKNTSEFMYLVALSDDTLAAVSYDN 241  
 DB 289 KEGFNATNEDTKKTCGLGEYWLGNDKISQLTRIGPTE--LLIENEDKGVKVAHHGG 346  
 QY 242 FWEDETRFEKMHILGRYSGNAGDAF---RGLKREDN---ONAMPFSTDVNDGCRPA 293  
 DB 347 FTVQTEANKYGVSVNKKYGTACNALMEGASQLVGENRFTWINGHFFSYDRDNDG--- 402  
 QY 294 CLYNGSVASCGHLNKTWMPNEGGLANLNGIHPSGL-----LATIGWGTWK 345  
 DB 403 -WYTTDPRQCSK-EDGGGMWYNRCHAMPNGRYWGLYSWMSKHGTDGVMWNV-- 458  
 QY 346 NNSPVKIKSVKMKIRMY 363  
 DB 459 KGSWISMRMSKIRPVF 476  
 RESULT 15  
 FIBB\_CHICK ID FIBB\_CHICK STANDARD; PRT; 463 AA.  
 AC 002020;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Fibrinogen beta chain precursor (contains: Fibrinopeptide B)  
 DE (Fragment).  
 GN FGB.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-13 AND 18-39.  
 RX MEDLINE=91182745; Pubmed=2009266;  
 RA Weissbach L., Oddoux C., Procyk R., Grlengier G.:  
 "The beta chain of chicken fibrinogen contains an atypical thrombin  
 cleavage site.";  
 RT Biochemistry 30:3290-3294(1991).  
 RL -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT  
 CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET  
 CC AGGREGATION.  
 CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS  
 CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.



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OM protein - protein search, using sw model

Run on: May 22, 2002, 15:08:30 ; Search time 29.86 Seconds  
(without alignments)  
1184.222 Million cell updates/sec

Title: US-09-596-196-9  
Perfect score: 2000  
Sequence: 1 EVVQNCVHSTDSVVNVIV.....PVKIKSVSMKIRMYNPK 368

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : PIR\_71: \*  
1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	413.5	20.7	439	2	fibrinogen-like pr
2	405.5	20.3	432	2	cytotoxic T-lympho
3	401.5	20.1	432	2	fibrinogen-like pr
4	397	19.9	312	2	fibrinogen-related
5	394.5	19.7	468	1	fibrinogen beta ch
6	375.5	18.8	491	1	fibrinogen beta ch
7	371.5	18.6	437	1	fibrinogen gamma-A
8	371.5	18.6	453	1	fibrinogen gamma-B
9	371.5	18.6	463	2	fibrinogen beta ch
10	370	18.5	479	2	fibrinogen gamma-B
11	365	18.2	444	2	fibrinogen gamma-B
12	360	18.0	432	1	fibrinogen gamma-B
13	352.5	17.6	438	2	fibrinogen gamma c
14	350.5	17.5	282	2	fibrinogen gamma c
15	348.5	17.4	774	2	scabrous locus (sc
16	346.5	17.3	328	2	fibrinogen beta ch
17	337.5	16.9	866	2	fibrinogen alpha c
18	330	16.5	1356	2	janusin precursor,
19	329	16.4	334	2	fibrinogen alpha c
20	328.5	16.4	641	1	fibrinogen alpha-I
21	327.5	16.4	1353	1	transferrin precurs
22	312	15.6	437	1	fibrinogen gamma-A
23	311.5	15.6	445	1	fibrinogen gamma-B
24	310.5	15.5	1810	1	tenascin-X bovin
25	310.5	15.5	1810	1	tenascin precursor
26	304.5	15.2	1914	2	tenascin Y precurs
27	303.5	15.2	326	2	fibrinogen alpha c
28	302.5	15.1	3566	1	tenascin-X precurs
29	302.5	15.1	440701	1	tenascin-X precurs

30	299	14.9	417	2	tenascin-X - pig (
31	296	14.8	220	2	tenascin homolog -
32	295	14.8	326	2	tenascin-X - pig
33	286	14.3	860	2	tenascin-X - mouse
34	284.5	14.2	2019	1	tenascin precursor
35	283.5	14.2	4006	2	tenascin precursor
36	282.5	14.1	1746	1	tenascin precursor
37	271	13.6	2201	2	tenascin-C - human
38	212.5	10.6	463	2	tenascin-C - human
39	180.5	9.0	915	2	hypothetical prote
40	180.5	9.0	927	2	hypothetical prote
41	173	8.7	431	2	hypothetical prote
42	154.5	7.7	933	2	cytoactin - chick
43	128.5	6.4	452	2	hypothetical prote
44	117	5.8	127	2	microfibril-associ
45	110.5	5.5	4588	2	dynein beta heavy

ALIGNMENTS

RESULT 1  
137391  
fibrinogen-like protein expressed in T lymphocytes (pt49) - human  
C:Species: Homo sapiens (man)  
C:Date: 01-Nov-1996 #sequence\_revision 01-Nov-1996 #text\_change 21-Jul-2000  
C:Accession: I37391; S47273  
R:Ruegg, C.; Pytel, R.  
Gene 160, 257-262, 1995  
A:Title: Sequence of a human transcript expressed in T-lymphocytes and encoding a fib  
A:Reference number: I37391; MUID:95369700  
A:Accession: I37391  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-439 <RES>  
A:Cross-references: EMBL:Z36531; NID:9535184; PID:CAA85298.1; PID:9535185  
A:Note: submitted to the EMBL Data Library, August 1994  
C:Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology  
F:210-435/Domain: fibrinogen beta/gamma homology <FBG>

Query Match	20.7%	Score 413.5	DB 2	Length 439
Best Local Similarity	30.2%	Pred. No. 2.9e-25		
Matches 119	Conservative 61	Mismatches 147	Indels 67	Gaps 15
QY	14	SSVNIIVEDGSNADESKNDYCKE	-----ESCQVYTK	50
Db	73	SRIEVEFKEVONLKEIVNSLKSC-QDCKIQADNDGDEGRGLLPSTGARGVDNRVR	131	
QY	51	ITREKHFMCNLONS-----IVSYTRSTKILRN	-----MDDQASLDLSNOVNEIM	100
Db	132	ELESFVNKLSSLEKAKEIIVLGRLEKLVNNNNIENVYDSKVAALTVVNSLDKRC	191	
QY	101	NRVLITTEVFRRKQDPFRRPVQSHGL-DCTDIKDTIGSVTPPSGLYIIRHGGSSYP	158	
Db	192	SKC-----PQEQIQSRPVQ-HILYKDCSDY	-----AIGRRSSFTYVTFDPKSS	237
QY	159	FEVMCDMDYRGCGWTIVQKIDGIIDFORLWCDYLDGFDLLGEFGLKIKPIYVQKN	218	
Db	238	FEVYCDMETMGCGWTVLQARLDGSTNFTWQDYKAGGNIRREFWLGNDRKIHLLT--KS	295	
QY	219	TSPMFLVLESEDDTLAAAYSDNFMLEDETRPFKMHIGRYSGNMGDAFRGLKKEDNQAM	278	
Db	296	KEMILRIDLEPNQVELALYDQFVAEFLKRLHVNNGYTGADALR-FNKHYNDLKL	354	
QY	279	PESTDVNDGCRPACTLVNGQSVKCSHLHNKGTGMWFECCGLANLG-IHFFSGKLATG	337	
Db	355	FETTPDKNDKRPSC-----NCG-LYSSSGMWFACLSANLNGYVYQKRGVANG	404	
QY	338	IQWGTW--TKNNSPVKIKSVSMKIRMYNP-YFK	368	
Db	405	IFWGTWPGVSEAHFGYKSSFEAKMIRPKHF	438	

RESULT 2  
A27447  
cytotoxic T-lymphocyte-specific protein precursor (clone p149) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 15-Dec-1988 #sequence\_revision 15-Dec-1988 #text\_change 03-Dec-1999  
C:Accession: A27447  
R:Koyama, T.; Hall, L.R.; Haser, W.G.; Tonegawa, S.; Saito, H.  
Proc. Natl. Acad. Sci. U.S.A. 84, 1609-1613, 1987  
A:Title: Structure of a cytotoxic T-lymphocyte-specific gene shows a strong homology to  
A:Reference number: A27447; MUID:87175527  
A:Accession: A27447  
A:Molecule type: mRNA  
A:Residues: 1-432 <KOY>  
A:Cross-references: GB:M16238; NID:g193304; PIDN:AAA37624.1; PID:g387156  
C:Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology  
F:203-428/Domain: fibrinogen beta/gamma homology <FBG>

Query Match 20.3%; Score 405.5; DB 2; Length 432;  
Best Local Similarity 35.4%; Pred. No. 1.2e-24;  
Matches 110; Conservative 43; Mismatches 115; Indels 43; Gaps 13;

QY 78 LNNMDEQA-----SLDLSNOVNELMNRVLLLTTEVRKOLD-----PPF 119  
DB 137 LNNMDEQA-----SLDLSNOVNELMNRVLLLTTEVRKOLD-----PPF 119  
QY 120 HRPVOSHGL-DCTDIKDTIGSVTKTPSGLYIIHEGSSYPPEVMCDMDYRGSGWTVIQK 177  
DB 195 SQPVQ-HLIIKPCSD-HYVLG---RRSSGAYVTDPHRRSSFEVYCDMETMGGWTVLDA 249  
QY 178 RIDGIIDFRLMCDYLDGFDLGEFWLGLKKIFYIVNOKNTSFMILYVALESEDDTLAVA 237  
DB 250 RIDGSTNFFREMKDYKAGGKLEREFWLGNDKIHLLT--KSKEMILRIDLEDFNGLTLYA 307  
QY 238 SYDNFMLEDETFEFKMHILGRYSGNMGDAFRGLKEDNOMAFSTSDVNDGCRACLVN 297  
DB 308 LYDQFYVANEFLKRYLHIGNYNGTGADALR-FSRHYNHDLREFTPDRDNDKYPGSG---- 362  
QY 298 GOSVSCSHLHNTKGTWMEFNEGLANLNG-IHPSGKLATGIGWGTWTKNN--SPVKIKS 354  
DB 363 -----NCG-LYSSSGWMEFNSCLANLNGKYVHQKYGVRNGLFWGTWPGINOAOPGKYKS 416  
QY 355 VSMKIRRMYNP 365  
DB 417 SFOAKMMIRP 427

RESULT 3  
I56934  
fibrinogen-like protein - mouse  
C:Species: Mus sp. (mouse)  
C:Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 03-Dec-1999  
C:Accession: I56934  
R:Parrr, R.L.; Fung, L.; Reneker, J.; Myers-Mason, N.; Leibowitz, J.L.; Levy, G.  
J. Virol. 69, 5033-5038, 1995  
A:Title: Association of mouse fibrinogen-like protein with murine hepatitis virus-induce  
A:Reference number: I56934; MUID:95333285  
A:Accession: I56934  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-432 <RES>  
A:Cross-references: GB:S78773; NID:g1042169; PIDN:AAB34823.1; PID:g1042170  
C:Gene: musfibp  
C:Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology  
F:203-428/Domain: fibrinogen beta/gamma homology <FBG>

Query Match 20.1%; Score 401.5; DB 2; Length 432;  
Best Local Similarity 35.0%; Pred. No. 2.6e-24;  
Matches 109; Conservative 43; Mismatches 116; Indels 43; Gaps 13;

QY 78 LNNMDEQA-----SLDLSNOVNELMNRVLLLTTEVRKOLD-----PPF 119  
DB 137 LNNMDEQA-----SLDLSNOVNELMNRVLLLTTEVRKOLD-----PPF 119  
QY 120 HRPVOSHGL-DCTDIKDTIGSVTKTPSGLYIIHEGSSYPPEVMCDMDYRGSGWTVIQK 177  
DB 195 SQPVQ-HLIIKPCSD-HYVLG---RRSSGAYVTDPHRRSSFEVYCDMETMGGWTVLDA 249  
QY 178 RIDGIIDFRLMCDYLDGFDLGEFWLGLKKIFYIVNOKNTSFMILYVALESEDDTLAVA 237  
DB 250 RIDGSTNFFREMKDYKAGGKLEREFWLGNDKIHLLT--KSKEMILRIDLEDFNGLTLYA 307  
QY 238 SYDNFMLEDETFEFKMHILGRYSGNMGDAFRGLKEDNOMAFSTSDVNDGCRACLVN 297  
DB 308 LYDQFYVANEFLKRYLHIGNYNGTGADALR-FSRHYNHDLREFTPDRDNDKYPGSG---- 362  
QY 298 GOSVSCSHLHNTKGTWMEFNEGLANLNG-IHPSGKLATGIGWGTWTKNN--SPVKIKS 354  
DB 363 -----NCG-LYSSSGWMEFNSCLANLNGKYVHQKYGVRNGLFWGTWPGINOAOPGKYKS 416  
QY 355 VSMKIRRMYNP 365  
DB 417 SFOAKMMIRP 427

RESULT 4  
JN0596  
fibrinogen-related protein HRPFP-1 precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 21-Jul-2000  
C:Accession: JN0596  
R:Yamamoto, T.; Gotoh, M.; Sasaki, H.; Terada, M.; Kitajima, M.; Hirohashi, S.  
Biochem. Biophys. Res. Commun. 193, 681-687, 1993  
A:Title: Molecular cloning and initial characterization of a novel fibrinogen-related  
A:Reference number: JN0596; MUID:93290661  
A:Accession: JN0596  
A:Molecule type: mRNA  
A:Residues: 1-312 <YAM>  
A:Cross-references: GB:D14446; NID:g939314; PIDN:BA03336.1; PID:g939315  
A:Experimental source: liver  
C:Superfamily: fibrinogen beta/gamma homology  
F:1-17/Domain: signal sequence #status predicted <SIG>  
F:18-312/Product: fibrinogen-related protein HRPFP-1 #status predicted <MAT>  
F:80-305/Domain: fibrinogen beta/gamma homology <FBG>

Query Match 19.9%; Score 397; DB 2; Length 312;  
Best Local Similarity 34.3%; Pred. No. 3.9e-24;  
Matches 111; Conservative 44; Mismatches 115; Indels 54; Gaps 12;

QY 67 IVSYRSTKLLRNMMDEQAASLDVLSNOVNELMNRVLLLTTEVRKOLD-----PPF 114  
DB 4 VSFILVTTALL--MGREISALEDCADQOMRLRAQVRLLETRVYQOQYKIKQLDQENEV 60  
QY 115 --LDPRHNPVQSHG-----LDCTDIKDTIGSVTKTPSGLYIIHEGSSYPPEVMCDMDY 167  
DB 61 QFLDKGDEDTVVDLGSKROYACSEIFNDGYKL---SSEFYIKIPLOQSAEESVYCDMS- 115  
QY 168 RGGGWTVIQRIDGIDFRLMCDYLDGFDLGEFWLGLKKIFYIVNOKNTSFMILY 224  
DB 116 DGGGWTVIQRIDGIDGSENFGRKMDYENGFGNIVQKHGEVWLGNDKIHLLTDEB--YTLK 173  
QY 225 VALESEDDTLAVAASVNDFMLEDETFEFKMHILGRYSGNMGDAFRGLKEDNQ-----NAMP 279  
DB 174 IDLADEKNSRYAQYKNFVGDENKNEYELNIEVSGTAGSLAGNHNPEQWMAASHQRMK 233  
QY 280 FSTSDVDNDCGRACLVNQSQVSCSHLHNTKGTWMEFNEGLANLNGIHHFSGKLLA---T 336  
DB 234 FSTWRDHDNYEGNCAEEDQS-----GWMFNCHSANLNGV--YSSPYTAKTDN 281  
QY 337 GIOWGTWTKNNSPVKIKSVMKIR 360  
DB 282 GIWVYTW--HGMWYSLKSYVMKIR 303

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RESULT 5
FGB0B
fibrinogen beta chain - bovine
N:Contains: fibrinopeptide B
C:Species: Bos primigenius taurus (cattle)
C>Date: 29-Jul-1981 #sequence-revision 29-Jul-1981 #text-change 13-Sep-1996
C:Accession: A03122, B03117, B37507, A37513, S02443
C:Blomback, B.; Doolittle, R.F.
Acta Chem. Scand. 17, 1816-1819, 1963
A:Title: The sequence of amino acids at the N-terminal end of bovine fibrinopeptide B.
A:Reference number: A03122
A:Accession: A03122
A:Molecule type: protein
A:Residues: 1-4 <BLO>
R:Sjoquist, J.; Blomback, B.; Wallen, P.
Ark. Kemi 16, 425-436, 1960
A:Title: Amino acid sequence of bovine fibrinopeptides.
A:Reference number: A03117
A:Accession: B03117
A:Molecule type: protein
A:Residues: 5-21 <SJO>
R:Martinelli, R.A.; Ingalls, A.S.; Rubira, M.R.; Hageman, T.C.; Hurrell, J.G.R.; Leach, S.
Arch. Biochem. Biophys. 192, 27-32, 1979
A:Title: Amino acid sequences of portions of the alpha and beta chains of bovine fibrinopeptides.
A:Reference number: A37507; M01D:9164394
A:Accession: B37507
A:Molecule type: protein
A:Residues: 22-53 <MAR>
R:Chung, D.W.; Rixon, M.W.; MacGillivray, R.T.A.; Davie, E.W.
Proc. Natl. Acad. Sci. U.S.A. 78, 1466-1470, 1981
A:Title: Characterization of a cDNA clone coding for the beta chain of bovine fibrinogen.
A:Reference number: A37513; M01D:81199473
A:Accession: A37513
A:Molecule type: mRNA
A:Residues: 44-468 <CHU>
R:Medved, L.V.; Platonova, T.N.; Litvinovich, S.V.; Lukinova, N.I.
FEBS Lett. 232, 56-60, 1988
A:Title: The cleavage of beta-chain in bovine fibrinogen D(H) fragment (95 kDa) leads to
A:Reference number: S02443; M01D:88211875
A:Accession: S02443
A:Molecule type: protein
A:Residues: 373-374 <MED>
C:Comment: Thrombin cleaves the bond between Arg-21 and Gly-22 to release fibrinopeptide B.
C:Superfamily: fibrinogen is a hexamer containing two sets of three nonidentical chains (alpha C, alpha 1, alpha 2).
C:Keywords: blood coagulation; glycoprotein; plasma; pyroglyutamic acid; sulfoprotein
F:76-205/Domain: fibrinogen disulfide ring homology <PDR>
F:215-464/Domain: fibrinogen beta/gamma homology <FBC>
F:1/Modified site: pyroglutamate carboxylic acid (Gln) #status experimental
F:6/Binding site: sulfate (Tyr) (covalent) #status experimental
F:21-22/Cleavage site: Arg-Gly (thrombin) #status experimental
F:371/Binding site: carboxylate (Asn) (covalent) #status predicted
F:372-373/Cleavage site: Arg-Thr (plasmin) #status experimental
Query Match 19.7%; Score 394.5; DB 1; Length 468;
Best Local Similarity 27.3%; Pred. No. 1e-23;
Matches 120; Conservative 54; Mismatches 145; Indels 117; Gaps 16;
Oy 7 CVHSTDSVNIIVEDSNKDESKSNDYCKEDSCSDVKTITREKHF--MCNRLQ 64
Db 72 CLHADPPLGLV-----CPMGCKADDTLVKQERPIKRSIEDLR 108
Oy 65 NSIVSYSTRSK-----LIRNMDEQOASLDYLSNQVNLNM----- 101
Db 109 NTVDSVSRSTSSSTFOYITLKNMKMGQNGQVQDNENYVNESSHLKHLQYIDFTVKNNI 168
Oy 102 -----RVLITTEVFRKQDLDP-----HRPQSHGLDCTDIKDTIGS 139
Db 169 PTKLRVLRSLIEILNRSKIOKLESVDSTOMEXCRTPCTVTCTNIPVVS--GKECEKILIRNDE 227

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RESULT 6
FGB0B
fibrinogen beta chain precursor [validated] - human
N:Alternate names: coagulation factor I
N:Contains: fibrinopeptide B
C:Species: Homo sapiens (man)
C>Date: 24-Apr-1984 #sequence-revision 31-Mar-1993 #text-change 08-Dec-2000
C:Accession: B43568; A90469; B90469; I37389; A94433; A90437; G54223; A03121;
R:Chung, D.W.; Harris, J.E.; Davie, E.W.
Adv. Exp. Med. Biol. 281, 39-48, 1990
A:Title: Nucleotide sequences of the three genes coding for human fibrinogen.
A:Reference number: A43568; M01D:91344740
A:Accession: B43568
A:Molecule type: DNA
A:Residues: 9-191, 'P', 193-491 <CHU>
R:Chung, D.W.; Que, B.G.; Rixon, M.W.; Mace Jr., M.; Davie, E.W.
Biochemistry 22, 3244-3250, 1983
A:Title: Characterization of complementary deoxyribonucleic acid and genomic deoxyribonucleic acid sequences of human fibrinogen.
A:Reference number: A90469; M01D:83283433
A:Accession: A90469
A:Molecule type: DNA
A:Residues: 1-38 <CHI>
A:Accession: B90469
A:Molecule type: mRNA
A:Residues: 9-191, 'A', 193-491 <CH2>
A:Cross-references: GB:J00129; NID:g182429; PIDN:AAA52429.1; PID:g182430
R:Huber, P.; Dalmont, J.; Courtois, G.; Laurent, M.; Assouline, Z.; Marguerie, G.
Nucleic Acids Res. 15, 1615-1625, 1987
A:Title: Characterization of the 5'-flanking region for the human fibrinogen beta gene.
A:Reference number: I37389; M01D:87146483
A:Accession: I37389
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-38 <HUB>
A:Cross-references: EMBL:X05018; NID:g31400; PIDN:CAA28674.1; PID:g31401
R:Henschen, A.; Lotspeich, F.; Southan, C.; Topfer-Petersen, E.
In: Protides of the Biological Fluids, Proc. 28th Colloq., Petersen, H., ed., pp.51-56,
A:Title: Human fibrinogen: sequence, sulfur bridges, glycosylation and some structural features.
A:Reference number: A94433
A:Contents: carbohydrate binding
A:Accession: A94433
A:Molecule type: protein
A:Residues: 31-137, 'OS', 140-144, 'OF', 147-491 <HEN>
R:Walt, K.W.K.; Takagi, T.; Doolittle, R.F.
Biochemistry 18, 68-76, 1979
A:Title: Amino acid sequence of the beta chain of human fibrinogen.
A:Reference number: A90437; M01D:79124640
A:Accession: A90437
A:Molecule type: protein
A:Residues: 31-144, 'OF', 147-231, 'D', 233-330, 'E', 332-491 <WAT>
R:Blomback, B.; Hessel, B.; Hogg, D.
Thromb. Res. 8, 639-658, 1976

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A:Residues: 27-437 <HEN>  
 R.Kant, J.A.; Lord, S.T.; Crabtree, G.R.  
 Proc. Natl. Acad. Sci. U.S.A. 80, 3953-3957, 1983  
 A:Title: Partial mRNA sequences for human Alpha, Beta, and gamma fibrinogen chains: ex  
 A:Reference number: A93956; MUID:83247396  
 A:Accession: B93956  
 A:Molecule type: mRNA  
 A:Residues: 276-437 <KAN>  
 R.Fornace Jr., A.J.; Cummings, D.E.; Comeau, C.M.; Kant, J.A.; Crabtree, G.R.  
 J. Biol. Chem. 259, 12826-12830, 1984  
 A:Title: Structure of the human gamma-fibrinogen gene. Alternate mRNA splicing near the  
 A:Reference number: A92448; MUID:85030379  
 A:Accession: B92448  
 A:Molecule type: DNA  
 A:Residues: 286-437 <FOR>  
 R.Riman, A.M.A.; Eaton, M.A.W.; Williamson, R.; Humphries, S.  
 Nucleic Acids Res. 11, 7427-7434, 1983  
 A:Title: Isolation and characterisation of cDNA clones for the Alpha- and gamma-chains  
 A:Reference number: 137393; MUID:84069777  
 A:Accession: 137393  
 A:Status: preliminary; translated from GB/EMBL/DDBJ  
 A:Molecule type: mRNA  
 A:Residues: 209-270 <RES>  
 A:Cross-references: EMBL:X00086; NID:g31445; PIDN:CAA24944.1; PID:9577055  
 R.Bertagnoli, M.E.; Beckerle, M.C.  
 J. Cell Biol. 121, 1329-1342, 1993  
 A:Title: Evidence for the selective association of a subpopulation of GPIIb-IIIa with th  
 A:Reference number: A40698; MUID:93286185  
 A:Accession: A40698  
 A:Molecule type: Protein  
 A:Residues: 27-33, 'XX', 36-41 <BER>  
 A:Experimental source: thrombin-activated platelets  
 R.Kunitake, S.T.; Carilli, C.T.; Lau, K.; Procter, A.A.; Naya-Vigine, J.; Kane, J.P.  
 Biochemistry 33, 1988-1993, 1994  
 A:Title: Identification of proteins associated with apolipoprotein A-I-containing lipop  
 A:Reference number: A54223; MUID:94162201  
 A:Accession: H54223  
 A:Molecule type: protein  
 A:Residues: 27-33, 'XX', 36-41 <KUN>  
 A:Note: Identification of tryptic peptides from high-density lipoproteins  
 R.Henschen, A.; Lotspelsch, F.; Kehl, M.; Southan, C.  
 Ann. N. Y. Acad. Sci. 408, 28-43, 1983  
 A:Title: Covalent structure of fibrinogen.  
 A:Reference number: A90037; MUID:83254370  
 A:Contents: annotation: review; disulfide bonds  
 R.Doolittle, R.F.; Takagi, T.; Watt, K.; Bouma III, H.; Cottrill, B.A.; Cassman, K.G.; G  
 In Regulatory Proteolytic Enzymes and Their Inhibitors, Magnusson, S., Ottesen, M., Folt  
 A:Title: The structures of fibrinogen and fibrin.  
 A:Reference number: A94437  
 A:Contents: annotation: disulfide bonds  
 R.Blomback, B.; Hessel, B.; Hoger, D.  
 Thromb. Res. 8, 639-658, 1976  
 A:Title: Disulfide bridges in NH-2-terminal part of human fibrinogen.  
 A:Reference number: A94309; MUID:83231455  
 A:Contents: annotation: disulfide bonds  
 R.Hoepflich, P.D.; Doolittle, R.F.  
 Biochemistry 22, 2049-2055, 1983  
 A:Title: Dimeric half-molecules of human fibrinogen are joined through disulfide bonds  
 A:Reference number: A90467; MUID:83231455  
 A:Contents: annotation: quaternary structure, disulfide bonds  
 R.Doolittle, R.F.  
 Annu. Rev. Biochem. 53, 195-229, 1984  
 A:Title: Fibrinogen and fibrin.  
 A:Reference number: A90041; MUID:84305751  
 A:Contents: annotation: review, EM structure, polymerization, ligands  
 R.Horvitz, B.H.; Varadi, A.; Scheraga, H.A.  
 Proc. Natl. Acad. Sci. U.S.A. 81, 5980-5984, 1984  
 A:Title: Localization of a fibrin gamma-chain polymerization site within segment Thr-374  
 A:Reference number: A94006; MUID:85014852  
 A:Contents: annotation: polymerization region  
 R.Kloczewiak, M.; Timmons, S.; Lukas, T.J.; Hawiger, J.  
 Biochemistry 23, 1767-1774, 1984

A:Title: Platelet receptor recognition site on human fibrinogen. Synthesis and struct  
 A:Reference number: A90483; MUID:84203545  
 A:Contents: annotation: platelet aggregation region  
 R.Plow, E.F.; Stroujl, A.H.; Meyer, D.; Marguerie, G.; Ginsberg, M.H.  
 J. Biol. Chem. 259, 5388-5391, 1984  
 A:Title: Evidence that three adhesive proteins interact with a common recognition sit  
 A:Reference number: A92477; MUID:84185664  
 A:Contents: annotation: platelet aggregation region  
 R.Dang, C.V.; Ebert, R.F.; Bell, W.R.  
 J. Biol. Chem. 260, 9713-9719, 1985  
 A:Title: Localization of a fibrinogen calcium binding site between gamma-subunit post  
 A:Reference number: A92549; MUID:85261382  
 A:Contents: annotation: calcium binding region  
 R.Kirschbaum, N.E.; Budzynski, A.Z.  
 J. Biol. Chem. 265, 13669-13676, 1990  
 A:Title: A unique proteolytic fragment of human fibrinogen containing the Alpha COOH  
 A:Reference number: A37117; MUID:90337977  
 A:Contents: annotation: hematin cleavage site  
 A:Note: The conversion of fibrinogen to fibrin is triggered by thrombin, which cle  
 A:Comment: The soft clot is converted into the hard clot by factor XIIIa (fibrin-stab  
 ger) and between alpha chains (weaker) of different monomers.  
 C:Comment: All fibrinogen chains are synthesized in the liver.  
 C:Comment: The two forms of gamma chain, A and B (see PIR:FGHGB), arise by alternate  
 intron, which makes this chain different from the gamma-B chain at positions 434-437  
 C:Genetics:  
 A:Gene: GDB:FGG  
 A:Cross-references: GDB:119132; OMIM:134850  
 A:Map position: 4q28-4q28  
 A:Introns: 26/3; 41/3; 103/7; 134/2; 178/1; 222/3; 284/2; 377/1; 433/3  
 A:Complex: The fibrinogen molecule is a hexamer containing two sets of alpha (see PIR  
 ins are contained in the core. Two three-chain coiled coils emerge from this core and  
 from the distal domain nodes.  
 C:Function:  
 A:Description: fibrinogen cleaved by thrombin yields monomers that are polymerized in  
 A:Pathway: blood coagulation  
 C:Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology  
 C:Keywords: alternative splicing; blood coagulation; calcium; coiled coil; glycoprote  
 F:1-26/Domain: signal sequence #status predicted <SIG>  
 F:27-437/Product: fibrinogen gamma-A chain #status experimental <MPN>  
 F:176-415/Domain: fibrinogen beta/gamma homology <BGB>  
 F:341-355/Domain: calcium binding #status predicted <CAB>  
 F:400-422/Region: polymerization site, binding to the amino end of the alpha chain of  
 F:423-437/Region: platelet aggregation #status predicted  
 F:34/Disulfide bonds: Interchain (to gamma-35) #status experimental  
 F:35/Disulfide bonds: Interchain (to gamma-34) #status experimental  
 F:45/Disulfide bonds: Interchain (to beta-110) #status experimental  
 F:49/Disulfide bonds: Interchain (to alpha-64) #status experimental  
 F:78/Binding site: carbohydrate (asn) (covalent) #status experimental  
 F:161/Disulfide bonds: Interchain (to beta-227) #status experimental  
 F:165/Disulfide bonds: Interchain (to alpha-180) #status experimental  
 F:179-208, 352-365/Disulfide bonds: #status experimental  
 F:424/Cross-link: isopeptide (Gln) (Interchain to Lys-432 N6-amino) #status experimen  
 F:432/Cross-link: isopeptide (Lys) (Interchain to Gln-424) #status experimental

Query Match 18.68; Score 371.5; DB 1; Length 437;  
 Best Local Similarity 31.9%; Pred. No. 6; Se-22;  
 Matches 105; Conservative 42; Mismatches 129; Indels 53; Gaps 11;

Qy 65 NSIYSYRSTKRLKLNMDQ-----QASIDYLSNQNVELMNRVLLTTEVFRKQDLP 118  
 Db 103 NMIDAATLKSRKMLEETIKYASITLTHDSITRYLQETIYNSNNQKIVNKEKV--AQLEAQ 160  
 Qy 119 PHRP-----VQSH-----GLDCTDIDKTSVTPSPSLIYIHPEGSSYPPEWCMDDYRGGG 171  
 Db 161 CQEPCKDVOVQHDITGKQCP-----IANKGAKOSGLYIRKLNQCPFLVYCEIDGSGNG 216  
 Qy 172 WTVYQKRIDGIIIDPQRLWCYLDGFGDI-----LGEFWLGLKFIYVQKNTSEMLYAL 227  
 Db 217 WTVFQKRIDGSDVPEKKNMIOYKEGFHSLPTGTTEFWLGNKRIHLISQSAIPALRVEL 276

```

Oy      228 ESEDDTLAASYNFNFMEDFTRFKMHGRRYS-GNAGCAFRLKKED-----NONAM 278
|       | : : : ||||| : : : |
Db      277 EDMMNGRTSTADYAMAFKXVCPPEADKRILTYAYFACGAGACAFAFDGFCDPDSDFKFTHSNCM 336
|       | : : : ||||| : : : |
Oy      279 PPTSDVDNDGCSPACLAVNGOSVSKSHLNKTGMWFNECCGLANIINGIHFFSGKL----- 333
|       | : : : ||||| : : : |
Db      337 QESTWMDNDKDFEGCNCEODGS-----GWMNMKCHAGHLNGVVYGQGTYSKAST 385
|       | : : : ||||| : : : |
Oy      334 ---LATGIOMGTWTCKNNSPVKIKSVSMKI 359
|       | : : : ||||| : : : |
Db      386 PNGDNGCIIATWTF--KTRWTSMTTKTMIKI 412
|       | : : : ||||| : : : |

RESULT      8
FGHUGB
fibrinogen gamma-B chain precursor [validated] - human
N:Alternate names: coagulation factor I; fibrinogen gamma-55 chain
C:Species: Homo sapiens (man)
C>Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 08-Dec-2000
C:Accession: A90494; A92448; A90453; A28203; B28203; J37390; A03126
R:Rixon, M.W.; Chung, D.W.; Davie, E.W.
Biochemistry 24, 2077-2086, 1985
A>Title: Nucleotide sequence of the gene for the gamma chain of human fibrinogen.
A:Reference number: A90494; MUID:85252774
A:Accession: A90494
A:Molecule type: DNA
A:Residues: 1-113,'I','115-453<RIX>
A:Cross-references: GB:M10014; GB:J00134; GB:J00135; GB:X00086; MID:g182438; PIDN:AAB595
R:Forname Jr., A.J.; Cummings, D.E.; Comeau, C.M.; Kant, J.A.; Crabtree, G.R.
J. Biol. Chem. 259, 12826-12830, 1984
A>Title: Structure of the human gamma-fibrinogen gene. Alternate mRNA splicing near the
A:Reference number: A92448; MUID:85030379
A:Accession: A92448
A:Molecule type: DNA
A:Residues: 286-453<FOR>
R:Mollenstein-Tedel, C.; Mossesson, M.W.
Biochemistry 20, 6146-6149, 1981
A>Title: Carboxy-terminal amino acid sequence of a human fibrinogen gamma-chain variant
A:Reference number: A90453; MUID:82068993
A:Accession: A90453
A:Molecule type: protein
A:Residues: 411-434,'Y',436-440,'Z','442','Z','444','B',446-447,'R',449,'ZBB',453<MOL>
R:Francis, C.W.; Mueller, E.; Henschel, A.; Simpson, P.J.; Marler, V.J.
Proc. Natl. Acad. Sci. U.S.A. 85, 3358-3362, 1988
A>Title: Carboxyl-terminal amino acid sequences of two variant forms of the gamma-chain
A:Reference number: A94194; MUID:88217900
A:Accession: A28203
A:Molecule type: protein
A:Residues: 433-449<FRA>
A:Accession: B28203
A:Molecule type: protein
A:Residues: 433-453<FR2>
R:Marchetti, L.; Zanelli, T.; Malcovati, M.; Tenchini, M.L.
DNA Seq. 1, 419-422, 1991
A>Title: Polymorphism of the human gamma chain fibrinogen gene.
A:Reference number: J37390; MUID:92119334
A:Accession: I37390
A>Status: translated from GB/EMBL/DDBT
A:Molecule type: mRNA
A:Residues: 75-286<RES>
A:Cross-references: EMBL:X51473; MID:g31410; PIDN:CAA35837.1; PID:g930064
C:Comment: The two forms of gamma chain, A (see PIR:FCHUG) and B, arise by alternate spli-
tron, which makes this chain different from the gamma-B chain at positions 434-437 and
C:Comment: The gamma-B chain is present in about 10% of the fibrinogen molecules in plas-
ma.
A:Gene: GDB:FGC
A:Cross-references: GDB:I19132; OMIM:134850
A:Map position: 4q28-q28
A:Introns: 26/3, 41/3, 103/1, 134/2, 178/1, 222/3, 284/2, 377/1
C:Complex: The fibrinogen molecule is a hexamer containing two sets of alpha (see PIR:FCG)
ins are contained in the core. Two three-chain coiled coils emerge from this core and con-
form the distal domain nodes.
;Function:

```

Query Match	Best Local Similarity	18.6%	Score 371.5	DB 1	Length 453
Matches 105; Conservative	42; Mismatches 129; Indels 53; Gaps 11;				
<p>A:Description fibrinogen cleaved by thrombin yields monomers that are polymerized in            A:Pathway: blood coagulation            C:Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology            C:Keywords: alternative splicing; blood coagulation; calcium; coiled coil; glycoprotein            F:1-26/Domain: signal sequence #status predicted &lt;SIG&gt;            F:27-45/Product: fibrinogen gamma-B chain #status experimental &lt;MP&gt;            F:176-415/Domain: fibrinogen beta/gamma homology &lt;B&gt;            F:341-355/Domain: calcium binding #status predicted &lt;CAB&gt;            F:400-422/Region: polymerization site; binding to the amino end of the alpha chain of            F:34/Disulfide bonds: interchain (to gamma-35) #status predicted            F:35/Disulfide bonds: interchain (to gamma-34) #status predicted            F:45/Disulfide bonds: interchain (to beta-110) #status predicted            F:749/Disulfide bonds: interchain (to alpha-64) #status predicted            F:78/Binding site: carbohydrate (Asn) (covalent) #status predicted            F:161/Disulfide bonds: interchain (to beta-227) #status predicted            F:179-208,352-365/Disulfide bonds: interchain (to alpha-180) #status predicted            F:424/Cross-Link: isopeptide (Gln) (interchain to Lys-432 N6-amino) #status predicted            F:432/Cross-Link: isopeptide (Lys) (interchain to Gln-424) #status predicted            F:432/Cross-Link: isopeptide (Lys) (interchain to Gln-424) #status predicted</p>					
Query Match	Best Local Similarity	18.6% <td>Score 371.5 <td>DB 1 <td>Length 453</td> </td></td>	Score 371.5 <td>DB 1 <td>Length 453</td> </td>	DB 1 <td>Length 453</td>	Length 453
Matches 105; Conservative	42; Mismatches 129; Indels 53; Gaps 11;				
Query Match	Best Local Similarity	18.6% <td>Score 371.5 <td>DB 2 <td>Length 463</td> </td></td>	Score 371.5 <td>DB 2 <td>Length 463</td> </td>	DB 2 <td>Length 463</td>	Length 463
Matches 112; Conservative	57; Mismatches 136; Indels 99; Gaps 17;				

```

OY 41 CEESCDVKITREKHF--MCRNLNSIYSY--TRSTKLLRNMMD----- 83
      | : : : : : : : : : : : : : : : : : : : : : : : :
DB 80 CPKGCETLTLLOEKYKRVLDLDRVAKFSSTSTTMQYVMDNKLKVTOKOKRDN 139
OY 84 -----EQOASLDYLSNOVNELMNRVLLLTTEVERKOLDPRHPVQS----- 125
      | : : : : : : : : : : : : : : : : : : : : : : : :
DB 140 DILSEVNTMELHYNVIRKNDLNNIPSSLRVLAVIDSL-HKKIOLENAIATQDYCR 198
OY 126 -----HGLDCTDIKDTIGSVTKPPSGLYIIHPBGSSYPEFVCMDDYRGCGWT 173
      | : : : : : : : : : : : : : : : : : : : : : : : :
DB 199 SPCVASCNIPVSGRECEDIYRKGET-----SEMYIIQPPPTTPPYRYCCMETEDNGSGWT 254
OY 174 VIQKRIDGIIIDFORLMDYLDGEG-----DLLGEFWLGKIKFIYVNGKNKNSFM 222
      | : : : : : : : : : : : : : : : : : : : : : : : :
DB 255 LIQNRDQSVNFGFRAMDEYRGRFENLAKSGGKKYCDTPGEGVLGNDKXISQLTGIPTK-- 312
OY 223 LYYALESED--DTLAYSYDNFWELEDETRFEKMHILGRYSGNAGDAF-----RGLKKEEDN- 274
      | : : : : : : : : : : : : : : : : : : : : : : : :
DB 313 --VLIEHEDNNGDKYS-ALYGGFTIHNEGNKYQLSVSNYKGNAGNALMEGASQLXGENRT 369
OY 275 ---QNAPESTSDVNDGCRPACLVNGQSVKCSHLLNKTGMFNECGLANLNGIHHSFG 331
      | : : : : : : : : : : : : : : : : : : : : : : : :
DB 370 MTIHNGMYFSTYDRDNDG-----WLTTPDRKQCSK-EDGGGMYNRCRHAANPNRGYYWGG 423
OY 332 KL-----LATGIQMGTWTKNNSPVKIKSVSKIRMYNPF 367
      | : : : : : : : : : : : : : : : : : : : : : : : :
DB 424 TYSMDAKHGTDDGIVMNM--KGSWYSMKKMSKIR---PYF 461

```

## RESULT 10

```

fibrinogen beta chain - sea lamprey (fragments)
N:Contains: fibrinopeptide B
C:Species: Petromyzon marinus (sea lamprey)
C>Date: 25-Oct-1987 #sequence_revision 19-Feb-1999 #text_change 13-Aug-1999
C:Accession: A25052; A03124; B03124
R:Bohonus, V. L.; Doollittle, R. F.; Pontes, M.; Strong, D. D.
Biochemistry 25, 6512-6516, 1986
A:Title: Complementary DNA sequence of lamprey fibrinogen beta chain.
A:Reference number: A25052; MUID:87076582
A:Accession: A25052
A:Molecule type: mRNA
A:Residues: 39-479 <BOH>
A:Cross-references: GB:M14773; NID:g213191; PIDN:AAA4261.1; PID:g213192
R:Coltell, B. A.; Doollittle, R. F.
Biochim. Biophys. Acta 453, 426-438, 1976
A:Title: Amino acid sequences of lamprey fibrinopeptides A and B and characterization of
A:Reference number: A03120; MUID:77065679
A:Accession: A03124
A:Molecule type: protein
A:Residues: 1-36 <COT1>
A:Accession: B03124
A:Molecule type: protein
A:Residues: 37-42 <COT2>
C:Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfide
C:Keywords: blood coagulation; glycoprotein; sulfoprotein
F:1-36/Product: fibrinopeptide B #status experimental <FBP>
F:37-479/Product: fibrin beta chain #status experimental <MAT>
F:29-77/Domain: fibrinogen beta/gamma homology <FBG>
F:13/Binding site: sulfate (Tyr) (covalent) #status experimental
F:27/Binding site: carbohydrate (asn) (covalent) #status experimental

```

## Query Match

18.5%: Score 370; DB 2; Length 479;  
Best Local Similarity 28.9%: Pred. No. 9.6e-22;

Matches 108; Conservative 63; Mismatches 137; Indels 66; Gaps 17;

```

OY 25 NAKESNSNDTVCKEDE-----ESCQVTKITREKHFMCNLDNSIYSYRS 73
      | : : : : : : : : : : : : : : : : : : : : : : : :
DB 130 NSFDRMASDNTLKNQVOTLRRRLNRSSTHVNAOKETENRYKEVKIR-IESTVAGSLRS 188

```

```

OY 74 TKLLRNMDQOASLDYLSNOVNELMNRVLLLTTEVERKOLDPRHPVQSHGLDCTDI 133
      | : : : : : : : : : : : : : : : : : : : : : : : :
DB 189 MKSVLEHRAKQNRBEAKIKQ-KELCSARCTVNRV-----PVVS-GHNCEDI 235
OY 134 KDTIGSVTKPPSGLYIIHPBGSSYPEFVCMDDYRGCGWTYIQKRIDGIIIDFORLMDYL 193
      | : : : : : : : : : : : : : : : : : : : : : : : :
DB 236 YRNGGRTSEA---YIOPDLFSEPKYKFCDEHSGSGMTVQNVRDSSNFARDMYTK 291
OY 194 DGFDDL-----GEFWLGKIKFIYVNGKNKNSFMALYALESDPDLAYSYDNF 242
      | : : : : : : : : : : : : : : : : : : : : : : : :
DB 292 AEFGNIAFGNKSICNINPEYWLGTGYVHQLTKQ-HTQOVLFSDMSDWSGVV-VAQVASF 349
OY 243 WLEDETRFEKMHILGRYSGNAGDA-FRGLK--EDNQ-----NAMPSTSDVNDGCRPAC 294
      | : : : : : : : : : : : : : : : : : : : : : : : :
DB 350 RPNDAQGYRLWVEDYSGNAGNALLEGATQLMGDRRTYTIHNGMFTFDRDNDWNP-- 407
OY 295 LVNGQSVKCSHLLNKTGMFNECGLANLNGIHHSFG---KLLA-----TGIQMGTWTKN 346
      | : : : : : : : : : : : : : : : : : : : : : : : :
DB 408 --GDPYKHCGR-EDAGGMYNRCRHAANPNRGYYWGGIYTKEQADYGTDDGVVMMNM--K 461
OY 347 NSPVKIKSVSKIR 360
      | : : : : : : : : : : : : : : : : : : : : : : : :
DB 462 GSWYSMRQAMKLR 475

```

## RESULT 11

```

fibrinogen gamma-B chain precursor - bovine
C:Species: Bos primigenius taurus (cattle)
C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 13-Aug-1999
C:Accession: S05313
R:Brown, W. M.; Dziegielewska, K. M.; Foreman, R. C.; Saunders, N. R.
Nucleic Acids Res. 17, 6397, 1989
A:Title: Nucleotide and deduced amino acid sequence of a gamma subunit of bovine fibrinogen
A:Reference number: S05313; MUID:89366676
A:Accession: S05313
A:Molecule type: mRNA
A:Residues: 1-444 <BRC>
A:Cross-references: EMBL:X15556; NID:g349; PIDN:CAA3562.1; PID:g350
A>Note: The authors translated the codon AGT for residue 105 as Ala and ATT for resid
C:Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-444/Product: fibrinogen gamma-B chain #status predicted <MAT>
F:174-414/Domain: fibrinogen beta/gamma homology <FBG>

```

## Query Match

18.2%: Score 365; DB 2; Length 444;  
Best Local Similarity 30.2%: Pred. No. 2.2e-21;

Matches 100; Conservative 51; Mismatches 124; Indels 56; Gaps 12;

```

OY 65 NSIYSYTSKTKLLRNMM-----DEQOASLDYLSNOVNELMNRVLLLTTEVERKOLDPRF 118
      | : : : : : : : : : : : : : : : : : : : : : : : :
DB 101 NNIESATKNSKSMEMEIKNYETLSTHSTREFLEEVYNSOKIVNLRDQV--OLEAN 158
OY 119 PHRPVQS-----HGLDCTDIKDTIGSVTKPPSGLYIIHPBGSSYPEFVCMDDYRGCG 171
      | : : : : : : : : : : : : : : : : : : : : : : : :
DB 159 COPEQDPIVKIHIDYGRQCD---YANKGAKESGIFLRPL-KAKQFLYVEIDGSGNG 213
OY 172 WTIVQKRIDGIIIDFORLMDYLDGFDLL-----GEFWLGKIKFIYVNGKNKNSFMALYV 225
      | : : : : : : : : : : : : : : : : : : : : : : : :
DB 214 WTVFQKRIDGSLDFKKNVIQYKEFGHISPTGTGMEFLGNEKIHLLISTQSSIPVLRT 273
OY 226 ALESDDPLAYSYDNFWELEDETRFEKMHILGRY-SGNAGDARGLKKEP-----NNN 276
      | : : : : : : : : : : : : : : : : : : : : : : : :
DB 274 QLEDNNGRTSTADYASFAVYTGENDRYRLYAYFICGDADADAGDYDFGDDSSDKFTFSN 333
OY 277 AMPFSTSDVNDGCRPACLVNGQSVKCSHLLNKTGMFNECGLANLNGIHHSFGKLAT 336
      | : : : : : : : : : : : : : : : : : : : : : : : :
DB 334 GMPFSTWSDNDKYGNC---AEQY-----GIGWMNKRCHAGHLNGLVYVYGGTYSKT 382
OY 337 -----GIQMGTWTKNNSPVKIKSVSKIR 359
      | : : : : : : : : : : : : : : : : : : : : : : : :
DB 383 STPNGYDNGIITATW--KSRWYSMKKTKTMIK 411

```



```
Db 58 KRISHPSPY-----RDCYDILQSC-SGQSPSPSGOYIYQPGGNC-IVYCOMMEIDEGM 110
Qy 173 TVIQRKIDGIDTDFORLMCDYLDGFGDILGCFWLGKTFYIYNQNTSFMLVVALESEDD 232
Db 111 TVFQRIDGIDTINFYKSMYSYOTGFGNLTFRMLGNDNIHYLSQGD--YELFVEIINTLG 168
Qy 233 TLVAASVDNFWLEDETREFKMLHIGRSGNAGDAFRGLKKEQNMAMPSTSDVDNDCGRP 292
Db 169 NHYIAKYNKFRIGDSFSEYLLVLGAYSGTAGDSL-----YHNTFRFSTYDNDND---- 218
Qy 293 ACLVNGQSVKSCSH-LHNKTCGMWNECGLANLNGIH-FSGKLLATGIQMGTFWTKNNSPV 350
Db 219 -----VYSINCASHSSYRGAMWYKSCLSLNLNGOYDYDYG---APSIYWSLTPGDND-- 268
Qy 351 KIKSVSMKIR 360
Db 269 QIPFAEMKLR 278
```

```
RESULT 15
A39832
scabrous locus (sca) proteIn precursor - fruit fly (Drosophila melanogaster)
C/Species: Drosophila melanogaster
C/Date: 31-Jan-1992 #sequence_revision 31-Jan-1992 #text_Change 01-Dec-2000
C/Accession: A39832; S58998
R:Baker, N.E.; Mlodzik, M.; Rubin, G.M.
Science 250, 1370-1377, 1990
A>Title: Spacing differentiation in the developing Drosophila eye: a fibrinogen-related
A/Reference number: A39832; MUID:91075223
A/Accession: A39832
A>Status: preliminary
A:Molecule type: mRNA
A/Residues: 1-774 <BAK>
A/Cross-references: GB:M60065; GB:M37703; NID:g158401; PID:g158402
R:Hu, X.; Lee, E.C.; Baker, N.E.
Genetics 141, 607-617, 1995
A>Title: Molecular analysis of scabrous mutant alleles from Drosophila melanogaster indi
A/Reference number: S58998; MUID:96109607
A/Accession: S58998
A>Status: preliminary
A:Molecule type: DNA
A/Residues: 1-18, 'T', 20-774 <HUX>
C/Genetics:
A:Gene: FlyBase:sca
A/Cross-references: FlyBase:FBgn0003326
A:Superfamily: fibrinogen beta/gamma homology
F:514-711/Domain: fibrinogen beta/gamma homology <FBG>
```

```
Query Match 17.4% Score 348.5; DB 2; Length 774;
Best Local Similarity 25.1% Pred. No. 9.2e-20;
Matches 100; Conservative 65; Mismatches 137; Indels 97; Gaps 14;
```

```
Qy 14 SSVNIVEDGSNAKDESKNDPTVCKEDCEESCDVTKIT-----REEKHFCRNLIQNSI 67
Db 360 TSMLELEDVGLQTKMKKSIPELRHEISKLEFFANAQITTSOSLIREGTNARSLSQAMA 419
Qy 68 VSYT-----RSTKRLRNMDQDQASLDYLSNOVNEIMNRVL----- 104
Db 420 VSVSVLQEREGMKRLSAN-VDQLRTNVDRLOSLVNDKMKNLTLNKPVRKRRPHNQVA 478
Qy 105 -----LITTEV-----FRKQLDPPRHPVOSHGLDCTDIKDTIGSVTKT 143
Db 479 QMPDDSPIDSVLAETLVSELENVETOYEAIINKLPH-----DCSEVH-----TOT 524
Qy 144 PSGLYIHREGSSYPFEVNCMDYRGGMVTVQKRIDGIDTDFORLMCDYLDGFGDILGEF 203
Db 525 -DGLHLIAPAGORHPLMHTCTAD-----GWTYQRRFDSADPNRSMADYAGSGFAGGEEF 579
Qy 204 WLGLKIFIVYNQNTSFMLVVALESEDDTLAASYDNFWLEDETFRFKMLHGRYSGNAG 263
Db 580 WIGNQQLHHLT--LDNCSRLQGVOMODIYDNVAVAEYKRFYISSRADGYRLHTAEYSGNAS 637
```

```
Qy 264 DAFRGLKKEQNMAMPSTSDVDNDCCRPACLVNGQSVKSCSHLHNKTCGMWNECGLANL 323
Db 638 DAL-----NYOQMGQFSAIDDDRDRIQTHCAANEFG-----GMWFSHCQHANL 680
Qy 324 NCIIHFSGLKLTATGIQMGTFWTKNNSPVKIKSVSMKIRRM 362
Db 681 NGRYNL-----GLTWPDARNEW-IAVKSRLMLVKRL 711
```

Search completed: May 22, 2002, 15:08:31  
Job time: 198 sec

**This Page Blank (uspto)**

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 22, 2002, 15:07:54 ; Search time 22.62 Seconds  
(without alignments)  
397.375 Million cell updates/sec

Title: US-09-596-196-9

Perfect score: 2000  
Sequence: 1 EVVQNCNCHSTDSVNVIV.....PVKIKSVSMKIRRMVNYFK 368

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

Issued\_Patents\_AA:\*  
1: /cgn2\_6/prodata/2/1aa/5A\_COMB.pep:\*  
2: /cgn2\_6/prodata/2/1aa/6A\_COMB.pep:\*  
3: /cgn2\_6/prodata/2/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/prodata/2/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/prodata/2/1aa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/prodata/2/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	425	21.2	491	2	US-08-933-821-4
2	425	21.2	491	3	US-08-960-507-4
3	425	21.2	491	4	US-09-136-828-4
4	405.5	20.3	490	4	US-08-740-223A-12
5	403.5	20.2	497	4	US-08-740-223A-4
6	402.5	20.1	497	1	US-08-373-579-4
7	402.5	20.1	497	2	US-08-418-595-4
8	402.5	20.1	497	2	US-08-665-926-4
9	402.5	20.1	497	2	US-08-348-492-4
10	402.5	20.1	497	4	US-09-162-437-4
11	400	20.0	493	2	US-08-933-821-2
12	400	20.0	493	3	US-08-960-507-2
13	400	20.0	493	4	US-09-136-828-2
14	399	19.9	312	1	US-08-525-505A-4
15	395.5	19.8	496	4	US-08-740-223A-22
16	395	19.8	478	4	US-08-740-223A-7
17	395	19.8	495	4	US-08-740-223A-26
18	395	19.8	498	4	US-08-740-223A-2
19	395	19.8	498	4	US-09-351-457-2
20	395	19.8	498	4	US-09-561-500-2
21	395	19.8	498	4	US-09-561-108-2
22	394	19.7	485	4	US-09-351-457-5
23	394	19.7	495	4	US-09-561-500-5
24	394	19.7	495	4	US-09-561-108-5
25	393	19.6	491	4	US-08-740-223A-13
26	389	19.4	314	1	US-08-525-505A-2
27	389	19.4	498	1	US-08-373-579-2

28	389	19.4	498	2	US-08-418-595-2	Sequence 2, Appl1
29	389	19.4	498	2	US-08-665-926-2	Sequence 2, Appl1
30	389	19.4	498	2	US-08-348-492-2	Sequence 2, Appl1
31	389	19.4	498	4	US-09-162-437-2	Sequence 2, Appl1
32	387.5	19.4	497	4	US-08-740-223A-14	Sequence 14, Appl1
33	381.5	19.1	480	4	US-08-740-223A-8	Sequence 8, Appl1
34	381.5	19.1	496	1	US-08-373-579-6	Sequence 6, Appl1
35	381.5	19.1	496	2	US-08-418-595-6	Sequence 6, Appl1
36	381.5	19.1	496	2	US-08-665-926-6	Sequence 6, Appl1
37	381.5	19.1	496	4	US-09-162-437-6	Sequence 6, Appl1
38	381.5	19.1	496	4	US-08-740-223A-6	Sequence 6, Appl1
39	381.5	19.1	496	4	US-09-351-457-4	Sequence 4, Appl1
40	381.5	19.1	496	4	US-09-561-500-4	Sequence 4, Appl1
41	381.5	19.1	496	4	US-09-561-108-4	Sequence 4, Appl1
42	381.5	19.1	499	4	US-08-740-223A-24	Sequence 24, Appl1
43	381	19.1	498	4	US-08-740-223A-20	Sequence 20, Appl1
44	379.5	19.0	346	3	US-08-960-507-19	Sequence 19, Appl1
45	375.5	18.8	491	1	US-08-206-176-4	Sequence 4, Appl1

#### ALIGNMENTS

```
RESULT 1
US-08-933-821-4
; Sequence 4, Application US/08933821
; Patent No. 5972338
; GENERAL INFORMATION:
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: The Ligands
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MinPath (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/933,821
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: P1130
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-3216
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-933-821-4

Query Match 21.2%; Score 425; DB 2; Length 491;
Best Local Similarity 26.9%; Pred. No. 2.5e-37;
Matches 119; Conservative 64; Mismatches 133; Indels 126; Gaps 14;

OY 24 SNADDESKNDYVKECEESCDYKTKITRE-EKHFMCRNQNIVSYTRSTKLLNNM 82
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 68 TKGDASTIKMTIRMDLENKIDVLSRKREIDVLAQVVDGNTVNEVKLLRRESNNM 127
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
OY 83 DE-QQASIDYV-----SNQYELMNRVLLTTE----- 109
   |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
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Db 128 SRVQLYQMLHEITRKRNLSLEQLNKILNVTTEMKMATRYRELEVKYASLTDLVN 187  
QY 110 -----VFRQ---LDP-----FPHRPVOSHGL----- 128  
Db 188 NOSVMTLLEEOCLRIFSRQDTHVSPPLVQVVPONHIPSQOYTRPGILGNEIORDPGYPR 247  
QY 129 DCTDKIDTIGSVTKRP-----SGLYTHHPGSSYPFEV 161  
Db 248 DLMPPDLATSTPKSPFKIPRYTFINEGPFKDCQAKKAGHSGVSGIYMKIPENSGPMQL 307  
QY 162 MCDMDYRGSGWTVIOKRIDGIDFORLWCDYLDGFGDLGFEWLGKIKFYIVNOKNTSF 221  
Db 308 WCNENSLDPGGMWTVIOKRTDGSVNFERNMENYKKGFONIDGEXWLGLENIYMLSNQDN--Y 365  
QY 222 MLYVALESDDTLAYASYDNFWLEDETRFEKMHILGRYSNAGADARGLKEDNQNAMPFS 281  
Db 366 KLLIELEMDSDKRYAEVSSFRLEPESEFYRLRLGTYYQGNADSMW-----HNGKOPT 419  
QY 282 TSDVDNDGCRPACLVNGQSVKCSHLNKTGMWPNCGLANLNGIHFGSKLLA---TGI 338  
Db 420 TIDRDKD-----MYAGNCAPH-KGWMYNAACHSNLNGVYRGCHYRSKHQDSI 468  
QY 339 QMGWTKNNSPVKIKSVSMKIR 360  
Db 469 FWAEEY--RGGSYSLRAVQMMIK 488

RESULT 2  
US-08-960-507-4  
; Sequence 4, Application US/08960507  
; Patent No. 6057435  
; GENERAL INFORMATION:  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; TITLE OF INVENTION: Tie Ligands  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Winpatlin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/960.507  
; FILING DATE:  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dreger, Ginger R.  
; REGISTRATION NUMBER: 33,055  
; REFERENCE/DOCKET NUMBER: P1130P1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-3216  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 491 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-08-960-507-4

Query Match 21.2%; Score 425; DB 3; Length 491;  
Best Local Similarity 26.9%; Pred. No. 2.5e-37;  
Matches 119; Conservative 64; Mismatches 133; Indels 126; Gaps 14;  
QY 24 SNAKESKNDPVCKDEDESCDVTKITRE-EKHFMCRNLGNSIVSYTRSKKLLRNMM 82  
: : | | : : | | : : | | : : | | : : | | : : | |

Db 68 TKGQDASTIKDMITRMDLENLKDYLRSQKREIDVLOLVYVDGNTVNEYKLLRKSRRNMN 127  
QY 83 DE-QGASLDYL-----SNQVNELMNRVLLTTE----- 109  
Db 128 SRVQLYQMLHEITRKRNLSLEQLNKILNVTTEMKMATRYRELEVKYASLTDLVN 187  
QY 110 -----VFRQ---LDP-----FPHRPVOSHGL----- 128  
Db 188 NOSVMTLLEEOCLRIFSRQDTHVSPPLVQVVPONHIPSQOYTRPGILGNEIORDPGYPR 247  
QY 129 DCTDKIDTIGSVTKRP-----SGLYTHHPGSSYPFEV 161  
Db 248 DLMPPDLATSTPKSPFKIPRYTFINEGPFKDCQAKKAGHSGVSGIYMKIPENSGPMQL 307  
QY 162 MCDMDYRGSGWTVIOKRIDGIDFORLWCDYLDGFGDLGFEWLGKIKFYIVNOKNTSF 221  
Db 308 WCNENSLDPGGMWTVIOKRTDGSVNFERNMENYKKGFONIDGEXWLGLENIYMLSNQDN--Y 365  
QY 222 MLYVALESDDTLAYASYDNFWLEDETRFEKMHILGRYSNAGADARGLKEDNQNAMPFS 281  
Db 366 KLLIELEMDSDKRYAEVSSFRLEPESEFYRLRLGTYYQGNADSMW-----HNGKOPT 419  
QY 282 TSDVDNDGCRPACLVNGQSVKCSHLNKTGMWPNCGLANLNGIHFGSKLLA---TGI 338  
Db 420 TIDRDKD-----MYAGNCAPH-KGWMYNAACHSNLNGVYRGCHYRSKHQDSI 468  
QY 339 QMGWTKNNSPVKIKSVSMKIR 360  
Db 469 FWAEEY--RGGSYSLRAVQMMIK 488

RESULT 3  
US-09-136-828-4  
; Sequence 4, Application US/09136828  
; Patent No. 6350450  
; GENERAL INFORMATION:  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; TITLE OF INVENTION: Tie Ligands  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Winpatlin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/136.828  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dreger, Ginger R.  
; REGISTRATION NUMBER: 33,055  
; REFERENCE/DOCKET NUMBER: P1130R1A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-3216  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 491 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-09-136-828-4

Query Match 21.2%; Score 425; DB 4; Length 491;  
Best Local Similarity 26.9%; Pred. No. 2.5e-37;



Matches 119; Conservative 64; Mismatches 133; Indels 126; Gaps 14;

QY 24 SNAKDESKNDYCKECCESCCKYKTKITRE-EKHFMCRNLONSIVYSTSTKLLNNM 82  
 Db 68 TKGODASTIDMTIRMDLENLKDVLRSOKREIDVLQVVDGNIIVNEVLLRKESHNM 127  
 QY 83 DE-QOASLDYL-----SNOVNEIMNRYLLLTTE----- 109  
 Db 128 SRVYQLYMOLLHEIRKRDNSLEISQLEKNITANTTEMLKMATRYRELEVYKASLTDLVN 187  
 QY 110 -----VERKO--LDP-----FPHRPVOSHGL----- 128  
 Db 188 NOSVMTILBEOCLRIHPSRODTHVSPPLYQVVPQHINSDQYTFGLGNETQDPCYPR 247  
 QY 129 DCDIDIKTISVYKTP-----SGLYIHPGSSYFEV 161  
 Db 248 DLMPPLPLSPKSPKIPKIPVTFINEGPKPCOAKAEAGHSVGIYMIKRENSNGPMOL 307  
 QY 162 MCDMDYGGGWTYQKRIIDGIDFQRLMCDYLDGFDLGEFNLGKIFIVYQKMTSF 221  
 Db 308 WCEMSLDPGGWTYQKRIIDGIDFQRLMCDYLDGFDLGEFNLGKIFIVYQKMTSF 221  
 QY 222 MLVVALESDDTLAYASYDNFWEDETRFFKMLGRYSNAGDAFRGLKKEDNONAMPFS 281  
 Db 366 KLIELEDWEDKRYAYLSEFRLPESEEFYRLGLTYQGNAGDSMM-----HNGKQFT 419  
 QY 282 TSDVDNCGCPACLVNQSVKSCSHLNKGTGWFNEGCLANGLNHHFSGKLA---TGI 338  
 Db 420 TLBDKQ-----MYAGNCNHFH-KGGMWYNACAHSLNGLVWYRGHYSRKHODGI 468  
 QY 339 QMGWTKNNSPVKIKSYSMKIR 360  
 Db 469 FMAEY--RGGSYSIRAYQMMIR 488

RESULT 4  
 US-08-740-223A-12  
 ; Sequence 12, Application US/08740223A  
 ; Patent No. 6265564  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Davis, et al.  
 ; TITLE OF INVENTION: Expressed Ligand - Vascular  
 ; TITLE OF INVENTION: Intercellular Signalling Molecule  
 ; NUMBER OF SEQUENCES: 28  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Regeneron Pharmaceuticals, Inc.  
 ; STREET: 777 Old Saw Mill Road  
 ; CITY: Tarrytown  
 ; STATE: NY  
 ; COUNTRY: USA  
 ; ZIP: 10591  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FastSeq Version 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/740, 223A  
 ; FILING DATE: 25-OCT-1996  
 ; CLASSIFICATION: 536  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: USSN 60/022/999  
 ; FILING DATE: 02-AUG-1996  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Cobert, Robert J  
 ; REGISTRATION NUMBER: 36,108  
 ; REFERENCE/DOCKET NUMBER: REG 333  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 914-345-7400  
 ; TELEFAX: 914-345-7721  
 ; INFORMATION FOR SEQ ID NO: 12:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 490 amino acids

TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 FEATURE:  
 NAME/KEY: hTLL  
 LOCATION: 1...490  
 OTHER INFORMATION: human TIE-2 ligand 1  
 US-08-740-223A-12

Query Match 20.3%; Score 405.5; DB 4; Length 490;  
 Best local similarity 27.5%; Pred. No. 3,3e-35;  
 Matches 118; Conservative 65; Mismatches 125; Indels 121; Gaps 16;

QY 3 VQNGCVHSTSDSVYNIIVEDGSSNAKDESKNDYCKECCESCCKYKTKITREKHFRCRN 62  
 Db 108 IQONAVQNHNT---ATMLEICTSLISQT-----AQTRRLFDVETQVNLQTSRLRIQL 156  
 QY 63 LQNSIVSY-----TRSTKKLLNNM 82  
 Db 157 LENSLSYKLEKQLQDTNELIKIHEKNSLLEHKLILEMEGKHKEIDTLKEEKENLQGLV 216  
 QY 83 DEQOASLDYLSNOVN-----ELM-----NRVLLTTEVF-----RKOLDPPF 119  
 Db 217 TRQTYIIIOELEKOLNKRATNNVYLQKQLELMQTVHNLCTEVLKGGKREEKRF- 275  
 QY 120 HRPVQSHGLDCTDIKDTIGSVTKTPSGLYIHPGSSYPFEVCMDDYRGCGWTYQKRI 179  
 Db 276 -----RQCADVY-----QAGFNKSGIYTYIINNMPKVFECNMDVNGGWTYQIHR 323  
 QY 180 DGIIDFORLMDYLDGFGDLDGEFNLGKIFIVYVQKNTSMFLVVALESDDTLAYASY 239  
 Db 324 DGSIDFQRMGEYKMGGBGSEYWLNEFLFALTQSR--QYMRILMDEGNRAVSQY 381  
 QY 240 DNFWLEDETRFFKMLGRYSNAGDAFRGLKKEDN--ONAMPFSTSDVDNCGCPAC--L 295  
 Db 382 DRFHIGNEKQNYRLXLGHGTGAG-----KQSSLLHAGDFSTKADNDNCKCKALM 434  
 QY 296 VNGQSVKSCSHLNKGTGWFNEGCLANGLNHFS-----GKLLATGIGWGTWTKNNSPVK 351  
 Db 435 LTG-----CWMFEDACPSNLNGMFWYAGONHGL--NGIKMYF--KGPSYS 477  
 QY 352 IKSYSMKIR 360  
 Db 478 IRSTTMMIR 486

RESULT 5  
 US-08-740-223A-4  
 ; Sequence 4, Application US/08740223A  
 ; Patent No. 6265564  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Davis, et al.  
 ; TITLE OF INVENTION: Expressed Ligand - Vascular  
 ; TITLE OF INVENTION: Intercellular Signalling Molecule  
 ; NUMBER OF SEQUENCES: 28  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Regeneron Pharmaceuticals, Inc.  
 ; STREET: 777 Old Saw Mill Road  
 ; CITY: Tarrytown  
 ; STATE: NY  
 ; COUNTRY: USA  
 ; ZIP: 10591  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FastSeq Version 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/740, 223A  
 ; FILING DATE: 25-OCT-1996  
 ; CLASSIFICATION: 536

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 60/022/999  
FILING DATE: 02-AUG-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Cobert, Robert J  
REGISTRATION NUMBER: 36,108  
REFERENCE/DOCKET NUMBER: REG 333  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 914-345-7400  
TELEFAX: 914-345-7721  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 497 amino acids  
TYPE: amino acid  
STRADEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
FEATURE:  
NAME/KEY: Human TIE-2 ligand 1  
LOCATION: 1...2146  
OTHER INFORMATION: from T98G clone  
US-08-740-223A-4

Query Match 20.2%; Score 403.5; DB 4; Length 497;  
Best Local Similarity 27.3%; Pred. No. 5.5e-35;  
Matches 117; Conservative 66; Mismatches 125; Indels 121; Gaps 16;

QY 3 VQNCVHSTSDSVNVIEDGSNARDESKNDTYCKEDCEESCDYKTKITREKHFMGRN 62  
DB 115 IQQNAVQNHNT---ATMEIGTSLSQT-----AEQTRKLTVDVETQVNLQTSLEIQL 163  
QY 63 LQNSTIVSY-----TRSTKLLRNMM 82  
DB 164 LENSISTYKLEKQLQOTNEILKIEHKNLSLEHKLIEGKHKEELDTLKEKENLQGLV 223  
QY 83 DEQQAISLYLSQNVN-----ELM-----NRVLLLTTEVF-----RKQLDPRP 119  
DB 224 TRQYITIOELEKQLRATNNNSVLOKQOLEMDYVHNVLCTKEVLLKGGKREEDKPF- 282  
QY 120 HRPVQSHGLDCTDIKDTIGSVTKPPSGLYIHPGSSYFPEVMCDMDYRGCGWTVIQKRI 179  
DB 283 -----RDCAADV-----QAGFNKSGIYITIIYINMPERKKVFCMDVNGGWTYIQHRE 330  
QY 180 DGIIDFQRLKCDYLDGFDLLGEFWLGLKTFIYVNOKNTSMLYVALESEDDTLAVASY 239  
DB 331 DGSIDFQGWKEYKMGFNPSPGSEYVLGNDFEFAITSQR--QYMLRIELMDWEGNRAVYSQY 388  
QY 240 DNFWEDETRPFKMHILGRYSNAGDAFRGLKEDN--QNAPFSTSDVNDGCRPAC--L 295  
DB 389 DRFHIGNEKQNTRLYLKCHTGTAG-----KQSSLILHGADEFSTKDDNDNCMKCKCALM 441  
QY 296 VNGQSVKSCSHLNKNTGWMFNECGLANLNGIHNFSG---KLLATGIGLOMGTWTKNNSPVK 351  
DB 442 LTG-----GWMFADACGSPSNLNCMFTYTAGQNHKRL--NGIKWHNF--KGPSYS 484  
QY 352 IKSVSKMIR 360  
DB 485 LRSTTMIR 493

US-08-373-579-4  
Sequence 4, Application US/08373579  
Patent No. 5650490  
GENERAL INFORMATION:  
APPLICANT: Davis, et al.  
TITLE OF INVENTION: TIE-2 LIGAND, METHOD OF MAKING AND USES  
TITLE OF INVENTION: THERBOF  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESSES:  
ADDRESS: Regeneron Pharmaceuticals, Inc.

STREET: 777 Old Saw Mill River Road  
CITY: Tarrytown  
STATE: New York  
COUNTRY: USA  
ZIP: 10591  
COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/373,579  
FILING DATE: 17-JAN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/353,503  
FILING DATE: 09-DEC-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/348,492  
FILING DATE: 02-DEC-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/330,261  
FILING DATE: 27-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/319,932  
FILING DATE: 07-OCT-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Cobert, Robert J.  
REGISTRATION NUMBER: 36,108  
REFERENCE/DOCKET NUMBER: REG 330-D  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (914) 345-7400  
TELEFAX: (914) 345-7721  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 497 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-373-579-4

Query Match 20.1%; Score 402.5; DB 1; Length 497;  
Best Local Similarity 27.3%; Pred. No. 7.1e-35;  
Matches 117; Conservative 66; Mismatches 125; Indels 121; Gaps 16;

QY 3 VQNCVHSTSDSVNVIEDGSNARDESKNDTYCKEDCEESCDYKTKITREKHFMGRN 62  
DB 115 IQQNAVQNHNT---ATMEIGTSLSQT-----AEQTRKLTVDVETQVNLQTSLEIQL 163  
QY 63 LQNSTIVSY-----TRSTKLLRNMM 82  
DB 164 LENSISTYKLEKQLQOTNEILKIEHKNLSLEHKLIEGKHKEELDTLKEKENLQGLV 223  
QY 83 DEQQAISLYLSQNVN-----ELM-----NRVLLLTTEVF-----RKQLDPRP 119  
DB 224 TRQYITIOELEKQLRATNNNSVLOKQOLEMDYVHNVLCTKEVLLKGGKREEDKPF- 282  
QY 120 HRPVQSHGLDCTDIKDTIGSVTKPPSGLYIHPGSSYFPEVMCDMDYRGCGWTVIQKRI 179  
DB 283 -----RDCAADV-----QAGFNKSGIYITIIYINMPERKKVFCMDVNGGWTYIQHRE 330  
QY 180 DGIIDFQRLKCDYLDGFDLLGEFWLGLKTFIYVNOKNTSMLYVALESEDDTLAVASY 239  
DB 331 DGSIDFQGWKEYKMGFNPSPGSEYVLGNDFEFAITSQR--QYMLRIELMDWEGNRAVYSQY 388  
QY 240 DNFWEDETRPFKMHILGRYSNAGDAFRGLKEDN--QNAPFSTSDVNDGCRPAC--L 295  
DB 389 DRFHIGNEKQNTRLYLKCHTGTAG-----KQSSLILHGADEFSTKDDNDNCMKCKCALM 441  
QY 296 VNGQSVKSCSHLNKNTGWMFNECGLANLNGIHNFSG---KLLATGIGLOMGTWTKNNSPVK 351  
DB 442 LTG-----GWMFADACGSPSNLNCMFTYTAGQNHKRL--NGIKWHNF--KGPSYS 484

QY 352 IKSVMKIR 360  
Db 485 LRSTTMIR 493

## RESULT 7

US-08-418-595-4  
: Sequence 4, Application US/08418595  
: Patent No. 5814464  
: GENERAL INFORMATION:  
: APPLICANT: Daviss, et al.  
: TITLE OF INVENTION: TIE-2 LIGAND, METHOD OF MAKING AND USES  
: TITLE OF INVENTION: THEREOF  
: NUMBER OF SEQUENCES: 6  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: Regeneron Pharmaceuticals, Inc.  
: STREET: 777 Old Saw Mill River Road  
: CITY: Tarrytown  
: STATE: New York  
: COUNTRY: USA  
: ZIP: 10591  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Floppy disk  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS  
: SOFTWARE: Patentln Release #1.0, Version #1.30  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/08/418,595  
: FILING DATE: 06-APR-1995  
: CLASSIFICATION: 435  
: PRIORITY APPLICATION DATA:  
: APPLICATION NUMBER: US 08/373,579  
: FILING DATE: 17-JAN-1995  
: APPLICATION NUMBER: US 08/353,503  
: FILING DATE: 09-DEC-1994  
: PRIORITY APPLICATION DATA:  
: APPLICATION NUMBER: US 08/348,492  
: FILING DATE: 02-DEC-1994  
: PRIORITY APPLICATION DATA:  
: APPLICATION NUMBER: US 08/330,261  
: FILING DATE: 27-OCT-1994  
: PRIORITY APPLICATION DATA:  
: APPLICATION NUMBER: US 08/319,932  
: FILING DATE: 07-OCT-1994  
: ATTORNEY/AGENT INFORMATION:  
: NAME: Cobert, Robert J.  
: REGISTRATION NUMBER: 36,108  
: REFERENCE/DOCKET NUMBER: REG 330-D  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: (914) 345-7400  
: TELEFAX: (914) 345-7721  
: INFORMATION FOR SEQ ID NO: 4:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 497 amino acids  
: TYPE: amino acid  
: TOPOLOGY: linear  
: MOLECULE TYPE: protein  
: US-08-418-595-4

Query Match 20.1%; Score 402.5; DB 2; Length 497;  
Best Local Similarity 27.3%; Pred. No. 7.1e-35;  
Matches 117; Conservative 66; Mismatches 125; Indels 121; Gaps 16;

QY 3 VQNCVHSTDSVVNIVEDSGSNADSKSNDTYCKEDCESCDVTKITREKHFMCN 62  
Db 115 IQQNAVQNH-----ATMLEIGTSLSGT-----AEQTRKLTDETVGLVNTSRLTIOL 163  
QY 63 LQNSIVS-----TRSTKILLRMM 82  
Db 164 LENSISTYLERKOLLQOTNETILKHEKNSLLEHKLLEMGKHKEBLDTLKEKENIOLIV 223

QY 83 DEQOASLDYLSNOVN-----ELM-----NRELLLTTEVF-----RKQDPFP 119  
Db 224 TRQYIIIOLEKQUNLRATNNNSVLQKQLELMDTVHNLVNLCTKEVLLGKKREEDRF- 282  
QY 120 HRPVQSHGLDCTDIKDTIGSVTKTPPSGLYITHPEGSSYPFEWCMDDYRGSGWTVIOKRI 179  
Db 283 -----RDCADYV-----QAGFNKSGIYTYIYNMPEPKKVFPCNMVDVNGSGWTVIOHRE 330  
QY 180 DGIIDFQRLKMDYLDGPFDDLGEFVLGKRTFYLYNOKNTSFMLYVALESDDTLATASY 239  
Db 331 DGSIDFQRMKEYKMGFGNPSGEYWLGNFTFATISQF--QYMLRIELMDWEGNRAVSQY 388  
QY 240 DNFMLEDTRPFKMHILGRYSGNAGDAFRLKEDN--ONAMPFSTVDNDGCRPAC--L 295  
Db 389 DRFHGNKQYRRLYKHTGTAG-----KQSLIHGADFSTKADADNOCCKCALM 441  
QY 296 VNGOSVKSCHLHNTGWMFNECGLANGLIHFS---GKLLATGIQWGTWTRNNSPVK 351  
Db 442 LTG-----GWMFADCGPSNLNGMEYTAGQNHGKL--NGIKWHYF--KGPSYS 484  
QY 352 IKSVMKIR 360  
Db 485 LRSTTMIR 493

## RESULT 8

US-08-665-926-4  
: Sequence 4, Application US/08665926  
: Patent No. 5851797  
: GENERAL INFORMATION:  
: APPLICANT: Valenzuela et al.  
: TITLE OF INVENTION: TIE LIGAND-3, METHODS OF MAKING AND USES  
: NUMBER OF SEQUENCES: 8  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: Regeneron Pharmaceuticals, Inc.  
: STREET: 777 Old Saw Mill River Road  
: CITY: Tarrytown  
: STATE: New York  
: COUNTRY: U.S.A.  
: ZIP: 10591-6707  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Floppy disk  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS  
: SOFTWARE: Patentln Release #1.0, Version #1.30  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/08/665,926  
: FILING DATE: 19-JUN-1996  
: CLASSIFICATION: 435  
: ATTORNEY/AGENT INFORMATION:  
: NAME: Robert J. Cobert  
: REGISTRATION NUMBER: 36,108  
: REFERENCE/DOCKET NUMBER: REG 330-H  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: (914) 345-7400  
: TELEFAX: (914) 345-2113  
: INFORMATION FOR SEQ ID NO: 4:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 497 amino acids  
: TYPE: amino acid  
: TOPOLOGY: linear  
: MOLECULE TYPE: protein  
: US-08-665-926-4

Query Match 20.1%; Score 402.5; DB 2; Length 497;  
Best Local Similarity 27.3%; Pred. No. 7.1e-35;  
Matches 117; Conservative 66; Mismatches 125; Indels 121; Gaps 16;

QY 3 VQNCVHSTDSVVNIVEDSGSNADSKSNDTYCKEDCESCDVTKITREKHFMCN 62  
Db 115 IQQNAVQNH-----ATMLEIGTSLSGT-----AEQTRKLTDETVGLVNTSRLTIOL 163



FILING DATE: 09-DEC-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/348,492  
FILING DATE: 02-DEC-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/330,261  
FILING DATE: 27-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/319,932  
FILING DATE: 07-OCT-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Cobert, Robert J.  
REGISTRATION NUMBER: 36,108  
REFERENCE/DOCKET NUMBER: REG 330-D  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (914) 345-7400  
TELEFAX: (914) 345-7721  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 497 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-162-437-4

Query Match 20.1%; Score 402.5; DB 4; Length 497;  
Best Local Similarity 27.3%; Pred. No. 7.1e-35;  
Matches 117; Conservative 66; Mismatches 125; Indels 121; Gaps 16;

3 VOGCVHSTGSSVNVNIDEDGSNAKDESKSNDYVCSEDCSCVKKTKITREKHFMCN 62  
115 IQQNAVQNHNT---ATMLEIGTSLLSQT-----AEOTKRLDVEYOVNLQTSRLQL 163  
63 LQNSIVSY-----TRSTFKRLRNMM 82  
164 LENSLSYFKLEKQLOQNTNELIKTHEKNSLEHNIKLEMEKGNKEBELDTLKREKENLQGLV 223  
83 DEQASLDYLSNOY-----ELM-----NRVLLLTVEF-----RKQDPEP 119  
224 TRQYIIIOELERKQNRATNTNSVLQKQLELMDTVHNLVNLCTKEVLLKGGKREEDKPF- 282  
120 HRPVQSHGLDCTDIKDTIGSVTKTPSGLYIINPREGSSYFPEVMDMDYRGSGMTVYQKRI 179  
283 -----RQCADYV-----QAGFNKSGIYTYIINMPERKAVFCGMADYNGSGMTVYQIRE 330  
180 DGIIDFORLWCDYLDGFGDILGEEFWLGIKLIYIVNOKNTSFMLYVALESEDDTLAVASY 239  
331 DGSIDFORGWKEYKMGFGNPSGEYWLGNFIFFAITSQR--OYMLRIELMDWEGNRAYSQY 388  
240 DNFULEDETRFEKMHLDGRYSNAGDAFRGLKEDN--QNAFPSTSDVDNDCGRPAC--L 295  
389 DRFDIGNKQNYRLYLGHGTAGC-----KQSSLLIHGADFSTKDDNDCNCKCKCALM 441  
296 VNGOSVSKSHLHKKTGWFNEGCSLANLGIHFS---GKLLATGIQMGTWTKNNSPVK 351  
442 LTG-----GMMFDACGSPNLTNGMFTYAGQNHGL--NGIKMHIF--KGPSYS 484  
352 IKSVMKIR 360  
485 LRSTTMMIR 493

RESULT 11  
US-08-933-821-2  
Sequence 2, Application US/08933821  
Patent No. 5972338  
GENERAL INFORMATION:  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
TITLE OF INVENTION: The Ligands  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/933,821  
FILING DATE:  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Dreger, Ginger R.  
REGISTRATION NUMBER: 33,055  
REFERENCE/DOCKET NUMBER: P1130  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-3216  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 493 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-933-821-2

Query Match 20.0%; Score 400; DB 2; Length 493;  
Best Local Similarity 31.9%; Pred. No. 1.3e-34;  
Matches 94; Conservative 50; Mismatches 93; Indels 58; Gaps 11;

97 NELMNRVLLTTEYFRKO-----LDPEPRVQSHGLDCTDIKDTIGSVTKTPSG----- 146  
221 NRINQI--STNEIQSDQNLKVLDPRLPTMPTLT-----SLPSTQKPSGPMWDC 278  
147 -----LYIHREGSSYFPEVMDMDYRGSGMTVYQKRIQKIDGIIIDFORLWCDYLD 194  
279 LQALEDHGDTSSIVLYKKEENTRMLQVWCDOHRPGGTVIQRRLDGSVNFPRMMEYKQ 338  
195 GFGDILGFEWGLIKKIEFYIVNOKNTSFMLYVALESEDDTLAVASYDNFWLDETRFEKMH 254  
339 GFGNIDGTYWGLENTIYTLNQG--YKLLVYMEDWSRKVFAEYASRLPESESYKLR 396  
255 LGRYSGNAGDAFRGLKEDNQNAMPFSTSDVDNDCGRPACLVNGOSVSKSHLHKKTGW 314  
397 LGRYHGNAGDSFTW-----HNGKQFTLLDRDHD-----VYTG--NCAH-YKGGGW 439  
315 FNEGGLANLNLGIHFSCKLLA---TGLOWGTWTKNNSPVKIKSVSMKIRRMATNPF 366  
440 YNACASHNLNGLWVYRGHYRSRYODGVYMAEF--RGGSYSLKVVYMMIRPNMTE 492

RESULT 12  
US-08-960-507-2  
Sequence 2, Application US/08960507  
Patent No. 6057435  
GENERAL INFORMATION:  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
TITLE OF INVENTION: The Ligands  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk



FILED DATE: 23-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: OBLON, NORMAN F.  
REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 4587-012-0 PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-413-3000  
TELEFAX: 703-413-2220  
INFORMATION FOR SEQ. ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 312 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-525-505A-4

Query Match 19.9%; Score 399; DB 1; Length 312;  
Best Local Similarity 34.3%; Pred. No. 8.1e-35;  
Matches 111; Conservative 44; Mismatches 115; Indels 54; Gaps 12;

QY 67 IVSTYSTKRLNMDEQASLDYLSNQVNEIMNRVLLITTEYFRKQ-----114  
DB 4 VFSFIIVTTALI--MGREISALEDCAQEQMRLRAQVRLLETRVKQCOQVRIKOLQENEV 60  
QY 115 --LDPPHRRPVQSHG-----LDCTDIKDTIGSVTKPPSGLYIHPRESSYFVEVCMQMDY 167  
DB 61 QPLDKGDENTVDLGSKROYADCESEIFNDGYKL---SGFYKIKPLOSPEFSSYCCMS- 115  
QY 168 RGGGWTVIQKRIDGIDFORLWCDYLDGFGDLL--GEFVLGLKIPYIYNOKNTSEMLY 224  
DB 116 DGGGWTVIQGRSDGSENFNGMKDYENGFCNPFYQKHGEYWLGNKNLHFLTQED--YTLK 173  
QY 225 VALESDDTLAVSYDNFMLEDETRFKMHLGRYSNAGDAFRGLKEDNO-----NAMP 279  
DB 174 IDLADFEKNSRYAQYKFKKYGDEKNEFELNIGESYSGTAGDSLGNFHPREVQWMAASHORMK 233  
QY 280 FSTSDVNDGCRPACLVNQGOSKCSHLHNKTKGWFNECGLANLGIHPSGKLLA---T 336  
DB 234 FSTWDRHDHNEGNCAEEDS-----GWFNRCSHANLNGV--YISGPTAKTDN 281  
QY 337 GIQMGTVTKNNSPYKIKSVSMKIR 360  
DB 282 GIWYTW--HGWMYSLKSVMKIR 303

RESULT 15  
US-08-740-223A-22  
Sequence 22, Application US/08740223A  
Patent No. 6265564  
GENERAL INFORMATION:  
APPLICANT: Davis, et al.  
TITLE OF INVENTION: Expressed Ligand - Vascular  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Regeneron Pharmaceuticals, Inc.  
STREET: 777 Old Saw Mill Road  
CITY: Tarrytown  
STATE: NY  
COUNTRY: USA  
ZIP: 10591  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/740,223A  
FILING DATE: 25-OCT-1996  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 60/022/999

FILED DATE: 02-AUG-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Coberly, Robert J.  
REGISTRATION NUMBER: 36,108  
REFERENCE/DOCKET NUMBER: REG 333  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 914-345-7400  
TELEFAX: 914-345-7721  
INFORMATION FOR SEQ. ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 496 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: Internal  
FEATURE:  
NAME/KEY: 2N2C1F (chimera 2)  
LOCATION: 1...496  
OTHER INFORMATION:  
US-08-740-223A-22

Query Match 19.8%; Score 395.5; DB 4; Length 496;  
Best Local Similarity 27.5%; Pred. No. 4.1e-34;  
Matches 116; Conservative 68; Mismatches 133; Indels 105; Gaps 17;

QY 3 VQNCVHHSTSDSSVNIIVEDGNSNAKDESKSDNYTCKEDCEBSCDVTKI---TREB---55  
DB 112 IQQNAVONQF---AVMIEIGTNLLNQF-----ABQTRKLDVQEAQVNLQTRLEQL 160  
QY 56 -KHFMCRN-LQNSIVSYSTRSTKL-----LNMMDEQASL 89  
DB 161 LEHSLSTNKLKQILDTQSTSEINKLQDKNSLEKVLAMEDKHIIQLOSLKEEKQDLVLV 220  
QY 90 DYLSNQVNEIMNRVLLIT--TEYFRKQ-----LDPPHRRPVQSH 126  
DB 221 SKQSIIELEKKIVTATVNNNSVLQKQHDLMETVNNLLTMSTNSAKDPTVAKEDQIS 280  
QY 127 GLDCTDIKDTIGSVTKPPSGLYIHPRESSYFVEVCMQMDYRGGGWTVIQKRIDGIDFQ 186  
DB 281 FRDCADYV---QAGFNKSGIYTIYINNMPDKPKVFCNMVDVNGGQWTVIOHREDGSLDFQ 336  
QY 187 RLWCDYLDGFGDLLGEFVLGLKIFEYIYNOKNTSEFMLYVALESDDTLAVASYDNFMLED 246  
DB 337 RQMKETKMGFGNPSGEYWLGNFIFALTQSR--QYMLRIELMDQEGNRAISQYDRFHIGN 394  
QY 247 ETRFKMHLGRYSNAGDAFRGLKEDN--ONAMPFSTSDVNDGCRPAC--LVNGOSVK 302  
DB 395 EKQNYRLYLKNGHTAG-----KQSSLIHGADFSYKADNDNCKCKALMLTG----443  
QY 303 SCSHLHNKKGWNECGLANLGIHPS---GLLATGIGMGTVTKNNSPYKIKSVSMK 358  
DB 444 -----GWFEDACGSPNLMGMYTAGQNHGKL--NGIKMHYF--KGPSYSLRSTTM 490  
QY 359 IR 360  
DB 491 IR 492

Search completed: May 22, 2002, 15:07:55  
Job time: 167 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

## OM protein - protein search, using sw model

Run on: May 22, 2002, 15:05:13 ; Search time 29.86 Seconds  
(Without alignments)  
1248.582 Million cell updates/sec

Title: US-09-596-196-4  
Perfect score: 2104  
Sequence: 1 MMSPSQASLLFLNVCIFICG.....PVKIKSVSMKIRMYNPYRK 388

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : PIR-71:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	413.5	19.7	439 2	fibrinogen-like pr
2	405.5	19.3	432 2	cytochrome b-lympho
3	401.5	19.1	432 2	fibrinogen-like pr
4	397	18.9	312 2	fibrinogen beta ch
5	394.5	18.8	468 1	fibrinogen beta ch
6	375.5	17.8	491 1	fibrinogen beta ch
7	371.5	17.7	437 1	fibrinogen beta ch
8	371.5	17.7	453 1	fibrinogen gamma-A
9	371.5	17.7	463 2	fibrinogen gamma-B
10	370	17.6	479 2	fibrinogen beta ch
11	365	17.3	444 2	fibrinogen beta ch
12	363	17.3	432 2	fibrinogen gamma-B
13	353	16.8	438 2	fibrinogen gamma-B
14	350.5	16.7	282 2	fibrinogen gamma C
15	348.5	16.6	774 2	scabrous locus (sc
16	346.5	16.5	328 2	fibrinogen beta ch
17	337.5	16.0	866 2	fibrinogen alpha c
18	330	15.7	1356 2	janusin precursor,
19	329	15.6	334 2	fibrinogen alpha c
20	328.5	15.6	641 1	fibrinogen alpha-I
21	327.5	15.6	1353 1	restictin precurs
22	312	14.8	323 2	transforming growt
23	311.5	14.8	437 1	fibrinogen gamma-A
24	311.5	14.8	445 1	fibrinogen gamma-B
25	311	14.8	4135 2	tenascin-X - bovin
26	310.5	14.8	1810 1	tenascin precursor
27	304.5	14.5	1914 2	tenascin Y precurs
28	303.5	14.4	326 2	tenascin-1 precursor
29	302.5	14.4	3566 1	tenascin-X precurs

30	299	14.2	417	2	S65944	tenascin-X - pig
31	296	14.1	220	2	S28170	tenascin homolog -
32	295	14.0	326	2	B47172	tenascin beta - pig
33	286	13.6	860	2	I48839	tenascin-X - mouse
34	284.5	13.5	2019	1	J01322	tenascin precursor
35	283.5	13.5	4006	2	T09070	proble tenascin
36	282.5	13.4	1746	1	S19694	tenascin precursor
37	271	12.9	2201	2	A32160	tenascin-C - human
38	212.5	10.1	463	2	T15876	hypothetical prote
39	180.5	8.6	915	2	T21773	hypothetical prote
40	180.5	8.6	927	2	T21772	hypothetical prote
41	173	8.2	431	2	T29850	cytoactin - chick
42	154.5	7.3	933	2	A31930	hypothetical prote
43	128.5	6.1	452	2	T26827	microfibril associ
44	117	5.6	127	2	FC2036	dynein beta heavy
45	110.5	5.3	4588	2	T28667	

## ALIGNMENTS

RESULT 1  
137391  
fibrinogen-like protein expressed in T lymphocytes (p149) - human  
C:Species: Homo sapiens (man)  
C:Date: 01-Nov-1996 #sequence\_revision 01-Nov-1996 #text\_change 21-Jul-2000  
C:Accession: I37391; S47273  
R:Ruegg, C.; Pytel, R.  
Gene 160, 257-262, 1995  
A:Title: Sequence of a human transcript expressed in T-lymphocytes and encoding a fib  
A:Reference number: I37391; MUID:9536700  
A:Accession: I37391  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-439 <RES>  
A:Cross-references: EMBL:Z36531; NID:9535184; PID:CA85298.1; PID:9535185  
A>Note: submitted to the EMBL Data Library, August 1994  
C:Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology  
F:210-435/Domain: fibrinogen beta/gamma homology <FBG>

Query Match	19.7%	Score 413.5;	DB 2;	Length 439;
Best Local Similarity	30.2%	Pred. No. 8.5e-25;		
Matches 119;	Conservative 61;	Mismatches 147;	Indels 67;	Gaps 15;
QY 34	SSVYNIIVEDGSMARDESKNDTVCKEDCE-----ESCQVYKTK 70			
DB 73	SRIVEVEREVONLKEIYNSLKSC-QDCKIQADNDGPRNGLLPSTGAGEVGDNRVR 131			
QY 71	ITREKHFMCNLDNS---IVSTRSTKILRM-----MDEQASLDYLSQVNEIM 120			
DB 132	ELESEVVKLSSELKNAREINVLHGRLEKLNLMNMIENYVDSKVNLFVNSLDGKC 191			
QY 121	NRVLLITTEVFRKQIDFPHRPVOSHGL--DCTDIKDTIGSVTPGSLVYIHREGSSYP 178			
DB 192	SKC-----PQEOIQSRPVQ-HLIYKDCSYR-----AIGKRSETRYVPDPKNS 237			
QY 179	FEVNCMDYRGGWTFVIOKRIIDGIIIDFQRLMCDYLDGFGDLGFWLGLKFIYVQKN 238			
DB 238	FEVVCDEMTGCGWTVLQARLDGSTNFTFMWQDYKAGFNLRFEPFWLGNXKHLLT--KS 295			
QY 239	TSEFVLVALESDDTLAYASTDNWLEDETFEFMHIGRTSGNAGDAFRGLAKKEDONAM 298			
DB 296	KEMILRIDLEDFNGVEVYALDYVYANEFKRYLHGVNNGTGDALR-FNKRYHNIDLK 354			
QY 299	PESTDVNDGCRACLVNGOSVSKSHLHKGTGMWNEGLANLG-IHFFSGKLATG 357			
DB 355	FTTPDKDNDRYPSG-----NCG-LYSSGWFDACLSAWLNKGYTHQKTRVNG 404			
QY 358	IOWGTW--TKNNSPVKIKSVSMKIRMYNP-YFK 388			
DB 405	IFWGTWPGVSEAHHPGKYSKFEKAKMMLRPHFK 438			

RESULT 2  
A27447  
cytotoxic T-lymphocyte-specific protein precursor (clone PT49) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 15-Dec-1988 #sequence\_revision 15-Dec-1988 #text\_change 03-Dec-1999  
C:Accession: A27447  
R:Koyama, T.; Hall, L.R.; Haser, W.G.; Tonegawa, S.; Salto, H.  
Proc. Natl. Acad. Sci. U.S.A. 84, 1609-1613, 1987  
A:Title: Structure of a cytotoxic T-lymphocyte-specific gene shows a strong homology to  
A:Reference number: A27447; MUID:87175527  
A:Accession: A27447  
A:Molecule type: mRNA  
A:Residues: 1-432 <RES>  
A:Cross-references: GB:M16228; NID:g193304; PIDN:AAA37624.1; PID:g387156  
C:Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology  
F:203-428/Domain: fibrinogen beta/gamma homology <FBG>

Query Match 19.3%; Score 405.5; DB 2; Length 432;  
Best Local Similarity 35.4%; Pred. No. 3.6e-24;  
Matches 110; Conservative 43; Mismatches 115; Indels 43; Gaps 13;

QY 98 LRNMDEQA-----SLDLSNQVNEIMNRVLLTTEVFRKLD-----PPF 139  
DB 137 LRNMDEQA-----SLDLSNQVNEIMNRVLLTTEVFRKLD-----PPF 139  
QY 140 HRPVSHGL--DCTDIKPTIGSVTPSGLYIHFGSSYPFEVACDMYRCGGWTVIOK 197  
DB 195 SQPVQ-HLIIKQCSD-HYVLG---RRSSGAVRVTPDHRNSSSEYVCDMETGGGTVIQA 249  
QY 198 RIDGIIDPQRLMCDYLDGFGDLGFEWLGKIFIVNOKNTSPMLYVALESDDTLAYA 257  
DB 250 RIDGSTNFTREKMDYKAGFGLNREFWLGNDIHLTL--KSEKMLRIDLEDFNGLTLYA 307  
QY 258 SYDNFWLEDETFEFKMHIGRYSGNAGDAFRGLKREDNQNAPEFSDVNDGCRACLVN 317  
DB 308 LYDQFYVANEFLKYLHLGNVINGTAGDALR-FSRHYNDLRFPTTDPDNDYPPSG---- 362  
QY 318 GQSVKSCSHLNKKTGMWNECGLANLNG-IHFSKLLATGIQGTWTKNN--SPVKIKS 374  
DB 363 -----NCG-LYSSGQWFDSCSLANLNGKYYHQKYGKVGNGIFMGTPGINGAOPGGYKS 416  
QY 375 VSMKIRMYNP 385  
DB 417 SEKQAKMIRP 427

RESULT 3  
156934  
fibrinogen-like protein - mouse  
C:Species: Mus sp. (mouse)  
C:Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 03-Dec-1999  
C:Accession: I56934  
R:Part, R.L.; Fung, L.; Reneker, J.; Myers-Mason, N.; Leibowitz, J.L.; Levy, G.  
J. Virol. 69, 5033-5038, 1995  
A:Title: Association of mouse fibrinogen-like protein with murine hepatitis virus-induce  
A:Reference number: I56934; MUID:95333285  
A:Accession: I56934  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-432 <RES>  
A:Cross-references: GB:S78773; NID:g1042169; PIDN:AAB34823.1; PID:g1042170  
C:Genetics:  
A:Gene: musfib1p  
C:Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology  
F:203-428/Domain: fibrinogen beta/gamma homology <FBG>

Query Match 19.1%; Score 401.5; DB 2; Length 432;  
Best Local Similarity 35.0%; Pred. No. 7.3e-24;  
Matches 109; Conservative 43; Mismatches 116; Indels 43; Gaps 13;

QY 98 LRNMDEQA-----SLDLSNQVNEIMNRVLLTTEVFRKLD-----PPF 139  
DB 137 LRNMDEQA-----SLDLSNQVNEIMNRVLLTTEVFRKLD-----PPF 139  
QY 140 HRPVSHGL--DCTDIKPTIGSVTPSGLYIHFGSSYPFEVACDMYRCGGWTVIOK 197  
DB 195 SQPVQ-HLIIKQCSD-HYVLG---RRSSGAVRVTPDHRNSSSEYVCDMETGGGTVIQA 249  
QY 198 RIDGIIDPQRLMCDYLDGFGDLGFEWLGKIFIVNOKNTSPMLYVALESDDTLAYA 257  
DB 250 RIDGSTNFTREKMDYKAGFGLNREFWLGNDIHLTL--KSEKMLRIDLEDFNGLTLYA 307  
QY 258 SYDNFWLEDETFEFKMHIGRYSGNAGDAFRGLKREDNQNAPEFSDVNDGCRACLVN 317  
DB 308 LYDQFYVANEFLKYLHLGNVINGTAGDALR-FSRHYNDLRFPTTDPDNDYPPSG---- 362  
QY 318 GQSVKSCSHLNKKTGMWNECGLANLNG-IHFSKLLATGIQGTWTKNN--SPVKIKS 374  
DB 363 -----NCG-LYSSGQWFDSCSLANLNGKYYHQKYGKVGNGIFMGTPGINGAOPGGYKS 416  
QY 375 VSMKIRMYNP 385  
DB 417 SEKQAKMIRP 427

RESULT 4  
JN0596  
fibrinogen-related protein HFRP-1 precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 21-Jul-2000  
C:Accession: JN0596  
R:Yamamoto, T.; Gotoh, M.; Sasaki, H.; Terada, M.; Kitajima, M.; Hirohashi, S.  
Biochem. Biophys. Res. Commun. 193, 681-687, 1993  
A:Title: Molecular cloning and initial characterization of a novel fibrinogen-related  
A:Reference number: JN0596; MUID:93290661  
A:Accession: JN0596  
A:Molecule type: mRNA  
A:Residues: 1-312 <YAM>  
A:Cross-references: GB:D14446; NID:g393314; PIDN:BA00336.1; PID:g393315  
A:Experimental source: liver  
C:Superfamily: fibrinogen beta/gamma homology  
F:1-17/Domain: signal sequence  
F:18-312/Product: fibrinogen-related protein HFRP-1  
F:80-305/Domain: fibrinogen beta/gamma homology <FBG>

Query Match 18.9%; Score 397; DB 2; Length 312;  
Best Local Similarity 34.3%; Pred. No. 1.1e-23;  
Matches 111; Conservative 44; Mismatches 115; Indels 54; Gaps 12;

QY 87 IVSYRSTKRLLRNMDEQA-----SLDLSNQVNEIMNRVLLTTEVFRKLD-----PPF 134  
DB 4 VESFLLVTTAL--MGREISALEDCAOEOMRLRAQVRLERVRVQOQVRIKOLQENEV 60  
QY 135 --LDLDFPHRPSVSHG-----LDCTDIKPTIGSVTPSGLYIHFGSSYPFEVACDMY 187  
DB 61 QFLDGDEDFVVDLSKROYADCSSEIFNDGYKL-----SGFYIKPLQSPAEFSVCDMS- 115  
QY 188 RCGWTVIOKRIIDGIIDPQRLMCDYLDGFGDL--GEFWLGKIFIVNOKNTSPMLY 244  
DB 116 DGGWTVIORSDGSENFGRGWKQYENGNGNIVQKHGEWLGKNTLHLTLQED--YTLK 173  
QY 245 VALESDDTLAYASYDNFWLEDETFEFKMHIGRYSGNAGDAFRGLKREDNQ-----NMP 299  
DB 174 IDLADFEEKSRYAQYKNEFVGDENFEYLINIEYSGTAGSLAGNHPHEVQWMAHSHQRMK 233  
QY 300 FSTSDVNDGCRACLAVNQSVKSCSHLNKKTGMWNECGLANLNGIHFSKLLA---T 356  
DB 234 FSTWDRDHNYEGNCAEEDQS-----GWFNRCHSANLNGV--YSSGPTTAKTDN 281  
QY 357 GIQGTWTKNNSPVKIKSVMKIR 380  
DB 282 GLVWYTW--HGMWYSILKSVMKIR 303

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RESULT 5
FGBOB
fibrinogen beta chain - bovine
N:Contains: fibrinopeptide B
C:Species: Bos primigenius taurus (cattle)
C>Date: 29-Jul-1981 #sequence-revision 29-Jul-1981 #text-change 13-Sep-1996
C:Accession: A031122; B031117; B37507; A37513; S02443
R:Blomback, B.; Doolittle, R.F.
Acta Chem. Scand. 17, 1816-1819, 1963
A:Title: The sequence of amino acids at the N-terminal end of bovine fibrinopeptide B.
A:Reference number: A031122
A:Accession: A031122
A:Molecule type: protein
A:Residues: 1-4 <BLD>
R:Sjogquist, J.; Blomback, B.; Wallen, P.
Ark. Kemi 16, 425-436, 1960
A:Title: Amino acid sequence of bovine fibrinopeptides.
A:Reference number: A03117
A:Accession: B03117
A:Molecule type: protein
A:Residues: 5-21 <SJO>
R:Martinelli, R.A.; Ingalls, A.S.; Rubira, M.R.; Hageman, T.C.; Hurrell, J.G.R.; Leach, S.
Arch. Biochem. Biophys. 192, 27-32, 1979
A:Title: Amino acid sequences of portions of the alpha and beta chains of bovine fibrin
A:Reference number: A37507; M01D:79164394
A:Accession: B37507
A:Molecule type: protein
A:Residues: 22-53 <MAR>
R:Chung, D.W.; Rixon, M.W.; MacGillivray, R.T.A.; Davie, E.W.
Proc. Natl. Acad. Sci. U.S.A. 78, 1466-1470, 1981
A:Title: Characterization of a cDNA clone coding for the beta chain of bovine fibrinogen
A:Reference number: A37513; M01D:81199473
A:Accession: A37513
A:Molecule type: mRNA
A:Residues: 44-468 <CHU>
R:Medved, L.V.; Platonova, T.N.; Litvinovich, S.V.; Lukinova, N.I.
FEBS Lett. 232, 56-60, 1988
A:Title: The cleavage of beta-chain in bovine fibrinogen D(H) fragment (95 kDa) leads to
A:Reference number: S02443; M01D:88211875
A:Accession: S02443
A:Molecule type: protein
A:Residues: 373-374 <MED>
C:Comment: Thrombin cleaves the bond between Arg-21 and Gly-22 to release fibrinopeptide
C:Comment: Fibrinogen is a hexamer containing two sets of three nonidentical chains (alpha
C:Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfid
C:Keywords: blood coagulation; glycoprotein; plasma; pyrrolidonic acid; sulfoprotein
F:76-205/Domain: fibrinogen disulfide ring homology <FBR>
F:215-464/Domain: fibrinogen beta/gamma homology <FBR>
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:5/Binding site: sulfate (Tyr) (covalent) #status experimental
F:21-22/Cleavage site: Arg-Gly (thrombin) #status experimental
F:371/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:372-373/Cleavage site: Arg-Thr (plasmin) #status experimental

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Query Match 18.8%; Score 394.5; DB 1; Length 468;
Best Local Similarity 27.5%; Pred. No. 2,9e-23;
Matches 120; Conservative 54; Mismatches 145; Indels 117; Gaps 16;

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QY 27 CVHSTDSSTVYVIVEDSSNAKDESKMDYCKEDSCDYKTKITREKHF--MCNLTQ 84
DB 72 CLHADPDLGLV-----CPTGCKIQLDTLVKQERPTKRSIEDLR 108
QY 85 NSIYSYTRSTFK-----LLRNMDDEQASLDYLSNOVNEILMN----- 121
DB 109 NTYVSVSTSSSTFQYITLKNMKKGRQNOVDENYVNESSLEKHQLYIDETVKNNT 168
QY 122 ----RVLLTTEYFRKQDPP-----HRPVSHGLDCTDIKDTIGS 159
DB 169 PTKLRVLRSLLENRSKIQKLESDVSTOMECRTPTCTVTCNIPVVS--GKECEKILRNEG 227

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QY 160 VTKPSGLYTHPESSYPPEVWCMDDYRGSGWTVIQKRIIDGIIIDPQLWCLYDGGFDL 219
DB 228 T-----SEMVLIDPEDESSKPRVRYCDMKTEKGMTVIQNRDGSGLDPFRKNDPVRKQGGNI 283
QY 220 L-----GEFWLGLKIKFYIVNOKNTSEFMYALESEDDTLAVSYNFWLEDE 267
DB 284 ATNAEGKKYCGVEYGLNDRIISQLTNMGPTK--LLIEMEDMKGDVYALYEGFTVQNE 341
QY 268 TRFFKMLGKRYSGNAGAF-----RGLKEDN-----QNAPEFSTSDVNDCCRACLVNGQ 319
DB 342 ANKYQLSVSKYKGTAGALLEGASQVLGENRMTIHSNMFSTYDRNDGDKTT-----D 396
QY 320 SVKSCSLHMKTGWMEFNECGLANINGIHFSGKL-----LATGLOMGTWTKNNSPVK 371
DB 397 PKQCSK-EDGGGWYRRCIAANPNNGRYNGAYTWDMAKHGTDGYYWMMW--QGSWYS 453
QY 372 IKSVSMKIRRMYPYF 387
DB 454 MKKSMKIR----PYF 465

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RESULT 6
FGBOB
fibrinogen beta chain precursor [validated] - human
N:Alternate names: coagulation factor I
N:Contains: fibrinopeptide B
C:Species: Homo sapiens (man)
C>Date: 24-Apr-1984 #sequence-revision 31-Mar-1993 #text-change 08-Dec-2000
C:Accession: B43568; A90469; B90469; I37389; A94433; A90437; A94309; G54223; A03121;
R:Chung, D.W.; Harris, J.E.; Davie, E.W.
Adv. Exp. Med. Biol. 281, 39-48, 1990
A:Title: Nucleotide sequences of the three genes coding for human fibrinogen.
A:Reference number: A43568; M01D:91344740
A:Accession: B43568
A:Molecule type: DNA
A:Residues: 9-191, 'P', 193-491 <CHU>
R:Chung, D.W.; Que, B.G.; Rixon, M.W.; Mace Jr., M.; Davie, E.W.
Biochemistry 22, 3244-3250, 1983
A:Title: Characterization of complementary deoxyribonucleic acid and genomic deoxyrib
A:Reference number: A90469; M01D:83283433
A:Accession: A90469
A:Molecule type: DNA
A:Residues: 1-38 <CHU>
A:Accession: B90469
A:Molecule type: mRNA
A:Residues: 9-191, 'A', 193-491 <CH2>
A:Cross-references: GB:J00129; NID:g182429; PIDN:AAA52429.1; PID:g182430
R:Huber, P.; Dalmont, J.; Courtois, G.; Laurent, M.; Assouline, Z.; Marguerie, G.
Nucleic Acids Res. 15, 1615-1625, 1987
A:Title: Characterization of the 5'-flanking region for the human fibrinogen beta gen
A:Reference number: I37389; M01D:87146483
A:Accession: I37389
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-38 <HUB>
A:Cross-references: EMBL:X05018; NID:g31400; PIDN:CAA28674.1; PID:g31401
R:Henschen, A.; Lottspeich, F.; Southan, C.; Topfer-Petersen, E.
In: Protides of the Biological Fluids, Proc. 28th Colloq., Peeters, H., ed., pp.51-56,
A:Title: Human fibrinogen: sequence, sulfur bridges, glycosylation and some structura
A:Reference number: A94433
A:Contents: carbohydrate binding
A:Accession: A94433
A:Molecule type: protein
A:Residues: 31-137, 'OS', 140-144, 'OF', 147-491 <HEN>
R:Walt, K.W.K.; Takagi, T.; Doolittle, R.F.
Biochemistry 18, 68-76, 1979
A:Title: Amino acid sequence of the beta chain of human fibrinogen.
A:Reference number: A90437; M01D:79124640
A:Accession: A90437
A:Molecule type: protein
A:Residues: 31-144, 'OF', 147-231, 'D', 233-330, 'E', 332-491 <WAT>
R:Blomback, B.; Hessel, B.; Hogg, D.
Thromb. Res. 8, 639-658, 1976

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A:Title: Disulfide bridges in NH-2-terminal part of human fibrinogen.  
A:Reference number: A94309; MUID:76225080  
A:Contents: disulfide bonds  
A:Accession: A94309  
A:Molecule type: protein  
R:Kunitake, S.T.; Carilli, C.T.; Lau, K.; Protter, A.A.; Naya-Vigne, J.; Kane, J.P.  
Biochemistry 33, 1988-1993, 1994  
A:Title: Identification of proteins associated with apolipoprotein A-I-containing lipoproteins  
A:Reference number: A54223; MUID:94162201  
A:Accession: G54223  
A:Molecule type: protein  
A:Residues: 164-174 <KUN>  
A:Note: Identification of tryptic peptides from high-density lipoproteins  
R:Henschen, A.; Lotzpeich, F.; Kehl, M.; Southan, C.  
Ann. N. Y. Acad. Sci. 408, 28-43, 1983  
A:Title: Covalent structure of fibrinogen.  
A:Reference number: A90037; MUID:83254370  
A:Contents: annotation; review; disulfide bonds  
R:Gardlund, B.; Hessel, B.; Marguerie, G.; Murano, G.; Blomback, B.  
Eur. J. Biochem. 77, 595-610, 1977  
A:Title: Primary structure of human fibrinogen. Characterization of disulfide-containing  
A:Reference number: A91249; MUID:77245999  
A:Contents: annotation; disulfide bonds  
R:Doolittle, R.F.; Takagi, T.; Watt, K.; Bouma, H.; Cottrell, B.A.; Cassman, K.G.; C  
in Regulatory Proteolytic Enzymes and Their Inhibitors, Magnusson, S., Ottesen, M., Fold  
A:Title: The structures of fibrinogen and fibrin.  
A:Contents: annotation; A94437  
A:Reference number: A94437  
R:Doolittle, R.F.  
Annu. Rev. Biochem. 53, 195-229, 1984  
A:Title: Fibrinogen and fibrin  
A:Reference number: A90041; MUID:84305751  
A:Contents: annotation; review, EM structure, polymerization, ligands  
R:Chung, D.W.; Rixon, M.W.; Que, B.G.; Davie, E.W.  
Ann. N. Y. Acad. Sci. 408, 449-456, 1983  
A:Title: Cloning of fibrinogen genes and their cDNA.  
A:Reference number: A90038; MUID:83254384  
A:Contents: annotation  
R:Kirschbaum, N.E.; Budzynski, A.Z.  
J. Biol. Chem. 265, 13669-13676, 1990  
A:Title: A unique proteolytic fragment of human fibrinogen containing the Alpha COOH-te  
A:Reference number: A37117; MUID:90337977  
A:Contents: annotation; hematin cleavage site  
A:Note: hematin, a protease from Haemertia ghilianii, the giant South American leech,  
C:Comment: The conversion of fibrinogen to fibrin is triggered by thrombin, which cleav  
ization sites responsible for the formation of the soft clot.  
C:Comment: The soft clot is converted into the hard clot by factor XIIIa (fibrin-stabiliz  
ger) and between alpha chains (weaker) of different monomers.  
C:Comment: All fibrinogen chains are synthesized in the liver.  
C:Genetics:  
A:Gene: GDB:FCB  
A:Cross-references: GDB:119130; OMIM:134830  
A:Map position: 4q28-4q28  
A:Introns: 38/3; 102/3; 164/1; 240/1; 278/1; 320/1; 415/2  
C:Complex: The fibrinogen molecule is a hexamer containing two sets of alpha (see PIR:FC  
ins are contained in the core. Two three-chain coiled coils emerge from this core and co  
from the distal domain nodes.  
C:Function:  
A:Description: fibrinogen cleaved by thrombin yields monomers that are polymerized into  
A:Pathway: blood coagulation  
C:Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfid  
C:Keywords: blood coagulation; coiled coil; glycoprotein; liver; plasma; pyroglyutamic ac  
F:1-30/Domain (or 4-30 or 15-30) signal sequence #status predicted <Sig>  
F:31-491/Product: fibrinopeptide B #status experimental <MAT>  
F:45-47/Product: fibrin beta chain #status experimental <APY>  
F:45-47/Region: polymerization site  
F:99-228/Domain: fibrinogen disulfide ring homology <FDR>  
F:228-487/Domain: fibrinogen beta/gamma homology <FBG>  
F:31/Modified site: pyroglutamate carboxylic acid (Glu) (in mature form) #status experimen  
F:44-45/Cleavage site: Arg-Gly (thrombin) #status experimental  
F:95/Disulfide bonds: Interchain (to alpha-55) #status experimental

F:106/Disulfide bonds: Interchain (to alpha-68) #status experimental  
F:110/Disulfide bonds: Interchain (to gamma-45) #status experimental  
F:223/Disulfide bonds: Interchain (to alpha-184) #status experimental  
F:227/Disulfide bonds: Interchain (to gamma-161) #status experimental  
F:231-316,241-270,424-437/Disulfide bonds: #status experimental  
F:394/Binding site: carbohydrate (asn) (covalent) #status experimental

Query Match 17.8%; Score 375.5; DB 1; Length 491;  
Best Local Similarity 26.6%; Pred. No. 9.6e-22;  
Matches 118; Conservative 56; Mismatches 142; Indels 127; Gaps 17;

QY 25 GNCVHSHDSSVNVNVEDGSSNAKDESKSNDYCKEDCESCYKRTITREEHFRCRLQ 84  
DB 93 GCCLHADPDLGLV-----CPTGCOLQALLOOE-----RPIR 124  
QY 85 NSI-----VSYTRSRK-----KLRLNMDEQASIDLYLSONVNLN----- 121  
DB 125 NSVDELNNVNEAVSOTSSSFQYMYLLKDLMOCKOKVAKDNENVNVEYSSELEKHQLYID 184  
QY 122 -----RVLLLTTEVFRKQLDPP-----HPPVQSHGLDCTD 152  
DB 185 ETVNSNIPTNLRLKSLILENLRSKIQKLESVDVSAQMEYCRPTCVSCNIPVVS-GKECEE 243  
QY 153 IKDTIGSYTKPTSGLYIIRPECCSIPFEVCMQDYRGSGWYIYQKRIDIDFQRLMCDY 212  
DB 244 IIRKGGET-----SEMYLIOPDSSVVRPYRYCDMNTENGMTVIQNRQDSYDFGRKMPY 299  
QY 213 LDGFGD-----LLGEFWLGLKFIYVNOKNTSFWLYALSEEDTFLAYASD 260  
DB 300 KCGFENVATNTDGRKYVCLPGEYWLGNDKISQITRMGPE--LLIEMEDKDKKXKANYG 357  
QY 261 NFWLEDETRFEFKMLGRYSGNADAFRG---LKKEDN---QNAPESTSDVDNDGCRP 312  
DB 358 GFTYONKAKYQISVNYKRYGTAGNALMDGASOLMGENRMTIHNGMFSTYDRNDG--- 414  
QY 313 ACLVNGQSVKSGSHLHNTGTMWFNECGLANLNGIHHSFKL-----LATGIOWGTWT 364  
DB 415 --WLTSDFRKQCK--EDGGGWNYNRCHANPNRGYWGQYTMADAKHGTDGGVVMWN- 470  
QY 365 KNSPVKIKSVSMKTRRMVNPYE 387  
DB 471 -KGSWYSMRKMSMKTR---PFF 488

RESULT 7  
FGHUG  
fibrinogen gamma-A chain precursor [validated] - human  
N:Alternate names: coagulation factor I  
C:Species: Homo sapiens (man)  
C:Date: 24-Apr-1984 #sequence\_revision 25-Feb-1985 #text\_change 08-Dec-2000  
C:Accession: A90470; B90494; C94433; B93956; B92448; I37393; A40698; H54223; A03125;  
R:Chung, D.W.; Chan, W.Y.; Davie, E.W.  
Biochemistry 22, 3250-3256, 1983  
A:Title: Characterization of a complementary deoxyribonucleic acid coding for the gam  
A:Reference number: A90470; MUID:83283434  
A:Accession: A90470  
A:Molecule type: mRNA  
A:Residues: 1-437 <CHU>  
R:Rixon, M.W.; Chung, D.W.; Davie, E.W.  
Biochemistry 24, 2077-2086, 1985  
A:Title: Nucleotide sequence of the gene for the gamma chain of human fibrinogen.  
A:Reference number: A90494; MUID:85252774  
A:Accession: B90494  
A:Molecule type: DNA  
A:Residues: 1-113, '1', 115-437 <RIX>  
R:Henschen, A.; Lotzpeich, F.; Southan, C.; Tofter-Petersen, E.  
in Proteins of the Biological Fluids, Proc. 28th Colloq., Peeters, H., ed., pp.51-56,  
A:Title: Human fibrinogen: sequence, sulfur bridges, glycosylation and some structura  
A:Reference number: A94433  
A:Accession: C94433  
A:Molecule type: protein

A:Residues: 27-437 <HEN>  
R.Kant, J.A.; Lord, S.T.; Crabtree, G.R.  
Proc. Natl. Acad. Sci. U.S.A. 80, 3953-3957, 1983  
A:Title: Partial mRNA sequences for human Alpha, Beta, and gamma fibrinogen chains: ex  
A:Reference number: A93956; M0ID:83247396  
A:Accession: B93956  
A:Molecule type: mRNA  
A:Residues: 276-437 <KAN>  
R.Fornace, Jr., A.J.; Cummings, D.E.; Comeau, C.M.; Kant, J.A.; Crabtree, G.R.  
J. Biol. Chem. 259, 12826-12830, 1984  
A:Title: Structure of the human gamma-fibrinogen gene. Alternate mRNA splicing near the  
A:Reference number: A92448; M0ID:85030379  
A:Accession: B92448  
A:Molecule type: DNA  
A:Residues: 286-437 <FOR>  
R.Fornace, Jr., A.J.; Cummings, D.E.; Comeau, C.M.; Kant, J.A.; Crabtree, G.R.  
Nucleic Acids Res. 11, 7427-7434, 1983  
A:Title: Isolation and characterization of cDNA clones for the Alpha- and gamma-chains  
A:Reference number: 137393; M0ID:84069777  
A:Accession: 137393  
A:Status: preliminary; translated from GB/EMBL/DDBB  
A:Molecule type: mRNA  
A:Residues: 209-270 <RES>  
A:Cross-references: EMBL:X00086; NID:g31445; PIDN:CAA24944.1; PID:g577055  
R.Bertagnoli, M.E.; Beckerle, M.C.  
J. Cell Biol. 121, 1329-1342, 1993  
A:Title: Evidence for the selective association of a subpopulation of GPIIb-IIIa with th  
A:Reference number: A40698; M0ID:93286185  
A:Accession: A40698  
A:Molecule type: protein  
A:Residues: 27-33, 'XX', 36-41 <BER>  
A:Experimental source: thrombin-activated platelets  
A:Note: sequence extracted from NCBI backbone (NCBIP:133734)  
R.Kuntake, S.T.; Carrilli, C.T.; Lau, K.; Protter, A.A.; Naya-Vigne, J.; Kane, J.P.  
Biochemistry 33, 1988-1993, 1994  
A:Title: Identification of proteins associated with apolipoprotein A-I-containing lipop  
A:Reference number: A54223; M0ID:94162201  
A:Accession: H54223  
A:Molecule type: protein  
A:Residues: 27-33, 'XX', 36-41 <KUN>  
A:Note: Identification of tryptic peptides from high-density lipoproteins  
R.Henschen, A.; Lottspeich, F.; Kehl, M.; Southan, C.  
Ann. N. Y. Acad. Sci. 408, 28-43, 1983  
A:Title: Covalent structure of fibrinogen.  
A:Reference number: A90037; M0ID:83254370  
A:Contents: annotation; review, disulfide bonds  
R.Doolittle, R.F.; Takagi, T.; Wolt, K.; Bouma III, H.; Cottrell, B.A.; Cassman, K.G.; G  
in Regulatory Proteolytic Enzymes and Their Inhibitors, Magnusson, S., Ottesen, M., Folt  
A:Title: The structures of fibrinogen and fibrin.  
A:Reference number: A94437  
A:Contents: annotation; disulfide bonds  
R.Blomback, B.; Hessel, B.; Hoger, D.  
Thromb. Res. 8, 639-658, 1976  
A:Title: Disulfide bridges in NH-2-terminal part of human fibrinogen.  
A:Reference number: A94309; M0ID:76225080  
A:Contents: annotation; disulfide bonds  
R.Hoeprich, P.D.; Doolittle, R.F.  
Biochemistry 22, 2049-2055, 1983  
A:Title: Dimeric half-molecules of human fibrinogen are joined through disulfide bonds  
A:Reference number: A90467; M0ID:83231465  
A:Contents: annotation; quaternary structure, disulfide bonds  
R.Doolittle, R.F.  
Annu. Rev. Biochem. 53, 195-229, 1984  
A:Title: Fibrinogen and fibrin.  
A:Reference number: A90041; M0ID:84305751  
A:Contents: annotation; review, EM structure, polymerization, ligands  
R.Horwitz, B.H.; Varadi, A.; Scheraga, H.A.  
Proc. Natl. Acad. Sci. U.S.A. 81, 5980-5984, 1984  
A:Title: Localization of a fibrin gamma-chain polymerization site within segment Thr-374  
A:Reference number: A94006; M0ID:85014892  
A:Contents: annotation; polymerization region  
R.Kloczewiak, M.; Timmons, S.; Lukas, T.J.; Hawiger, J.  
Biochemistry 23, 1767-1774, 1984

A:Title: Platelet receptor recognition site on human fibrinogen. Synthesis and struct  
A:Reference number: A90483; M0ID:84203545  
A:Contents: annotation; platelet aggregation region  
R.Plow, E.F.; Stoull, A.H.; Meyer, D.; Marguerite, G.; Ginsberg, M.H.  
J. Biol. Chem. 259, 5388-5391, 1984  
A:Title: Evidence that three adhesive proteins interact with a common recognition sit  
A:Reference number: A92477; M0ID:84185664  
A:Contents: annotation; platelet aggregation region  
R.Dang, C.V.; Ebert, R.F.; Bell, W.R.  
J. Biol. Chem. 260, 9713-9719, 1985  
A:Title: Localization of a fibrinogen calcium binding site between gamma-subunit posi  
A:Reference number: A92549; M0ID:85261382  
A:Contents: annotation; calcium binding region  
R.Kirschbaum, N.E.; Budzynski, A.Z.  
J. Biol. Chem. 265, 13669-13676, 1990  
A:Title: A unique proteolytic fragment of human fibrinogen containing the Alpha COOH  
A:Reference number: A37117; M0ID:90337977  
A:Contents: annotation; hematin cleavage site  
A:Note: hementin, a protease from Haemolysis, the giant South American lee  
C:Comment: The conversion of fibrinogen to fibrin is triggered by thrombin, which cle  
ization sites responsible for the formation of the soft clot.  
C:Comment: The soft clot is converted into the hard clot by Factor XIIIa (fibrin-stab  
ger) and between alpha chains (weaker) of different monomers.  
C:Comment: All fibrinogen chains are synthesized in the liver.  
C:Comment: The two forms of gamma chain, A and B (see PIR:FGHUGB), arise by alternate  
intron, which makes this chain different from the gamma-B chain at positions 434-437  
C:Genetics:  
A:Gene: GDB:FGG  
A:Cross-references: GDB:119132; OMIM:134850  
A:Map position: 4q28-4q28  
A:Introns: 26/3; 41/3; 103/4; 134/2; 178/1; 222/3; 284/2; 377/1; 433/3  
C:Complex: The fibrinogen molecule is a hexamer containing two sets of alpha (see PIR  
ins are contained in the core. Two three-chain coiled coils emerge from this core and  
from the distal domain nodes.  
C:Function:  
A:Description: fibrinogen cleaved by thrombin yields monomers that are polymerized in  
A:Pathway: blood coagulation  
C:Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology  
F:1-26/Domain: signal sequence #status predicted <SIG>  
F:27-437/Product: fibrinogen gamma-A chain #status experimental <MPR>  
F:176-415/Domain: fibrinogen beta/gamma homology <FBG>  
F:341-355/Domain: calcium binding #status predicted <AB>  
F:400-422/Region: polymerization site, binding to the amino end of the alpha chain of  
F:423-437/Region: platelet aggregation #status predicted  
F:34/Disulfide bonds: Interchain (to gamma-35) #status experimental  
F:35/Disulfide bonds: Interchain (to gamma-14) #status experimental  
F:45/Disulfide bonds: Interchain (to beta-110) #status experimental  
F:49/Disulfide bonds: Interchain (to alpha-64) #status experimental  
F:78/Binding site: carbohydrate (asn) (covalent) #status experimental  
F:161/Disulfide bonds: Interchain (to beta-227) #status experimental  
F:165/Disulfide bonds: Interchain (to alpha-180) #status experimental  
F:179-208, 352-365/Disulfide bonds: #status experimental  
F:424/Cross-link: isopeptide (Gln) (interchain to Lys-432 N6-amino) #status experimen  
F:432/Cross-link: isopeptide (Lys) (interchain to Gln-424) #status experimental

Query Match	17.7%	Score 371.5;	DB 1;	Length 437;
Best Local Similarity	31.9%	Pred. No. 1.7e-21;		
Matches 105;	Conservative 42;	Mismatches 129;	Indels 53;	Gaps 11;
QY	85	NSIYSYRSTRKLLRNMMDEQ-----QASLDYLSNOVNEIMRNVLTLTTEVFRKQIDPF	138	
DB	103	NMIDAATLRSKRLLEIMTKYEASLITLHDSSTPGLYIYNSSNNQIVMLKEVY--AQLEAQ	160	
QY	139	PHRP-----VQSH---GLDCTDIDKDTIGSVTRKPSGLYIIPEGSSYFEVWCMDYGGG	191	
DB	161	QGECKRFPVQIHDTGGDCQD---IANKAKGSGLFIPIKRNQGFVYCEIDSSGNG	216	
QY	192	WTVYQKRIDGIDFQRLMCDYLDGFGDL---LGEFWLGLKTFYIVNQKNTSEFMVAL	247	
DB	217	WTVYQKRIDGSDVPRKKNWVIQYKGEFGHLSPTGTEFWLGNKIHLLISTQAIPIALRYEL	276	

```

Oy 248 ESEDDILAVASDNDNLEDETRFEFMHLGRYS-GAAGAPFGLKKED-----NQAM 298
Db 277 EDWNGRISTADYAMKRVPEADKYRLTYAYFAGDAGAFGDFGDDPSDKFPTSHNGM 336
Oy 299 PESTSDVYNDNCRCRAPCLVNGOSVKSCHLHNKTKGWFMFEGCGLANLNGIHFSGKL----- 353
Db 337 QESTWDDNDNDFEGGCAQODS-----GMMNMKKHAGHLNGVYQGCTYKAST 385
Oy 354 ---LATGIQWGTWTKNNSPVKIKSVSMKI 379
Db 386 PNGYDNGITWATW--KTRWYSMKTKTKMI 412

RESULT 8
FGHUGB
Fibrinogen gamma-B chain precursor [validated] - human
N:Alternate names: coagulation factor I; fibrinogen gamma-55 chain
C:Species: Homo sapiens (man)
C>Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 08-Dec-2000
C:Accession: A90444; A92448; A90453; A28203; B28203; I37390; A03126
R:Rixom, M.W.; Chung, D.W.; Davie, E.W.
Biochemistry 24, 2077-2086, 1985
A:Title: Nucleotide sequence of the gene for the gamma chain of human fibrinogen.
A:Reference number: A90494; MUID:85252774
A:Accession: A90494
A:Molecule type: DNA
A:Residues: 1-113,'I',115-453 <RIX>
A:Cross-references: GB:M0014; GB:J00134; GB:J00135; GB:X00086; NID:g182438; PIDN:AMB5995
R:Ropane Jr., A.J.; Cummings, D.E.; Comeau, C.M.; Kant, J.A.; Crabtree, G.R.
J. Biol. Chem. 259, 12826-12830, 1984
A:Title: Structure of the human gamma-fibrinogen gene. Alternate mRNA splicing near the
A:Reference number: A92448; MUID:85030379
A:Accession: A92448
A:Molecule type: DNA
A:Residues: 286-453 <FOR>
R:Wolfenstein-Todel, C.; Mossesson, M.W.
Biochemistry 20, 6146-6149, 1981
A:Title: Carboxy-terminal amino acid sequence of a human fibrinogen gamma-chain variant
A:Reference number: A90453; MUID:82068993
A:Accession: A90453
A:Molecule type: protein
A:Residues: 411-434,'Y',436-440,'Z',442,'Z',444,'B',446-447,'R',449,'ZBB',453 <NOL>
R:Francis, C.W.; Mueller, E.; Henschen, A.; Simpson, P.J.; Warder, V.J.
Proc. Natl. Acad. Sci. U.S.A. 85, 3358-3362, 1988
A:Title: Carboxyl-terminal amino acid sequences of two variant forms of the gamma-chain
A:Reference number: A94194; MUID:88217900
A:Accession: A28203
A:Molecule type: protein
A:Residues: 433-449 <FRA>
A:Accession: B28203
A:Molecule type: protein
A:Residues: 433-453 <FRZ>
R:Marchetti, L.; Zanelli, T.; Malcovati, M.; Tenchini, M.L.
DNA Seq. 1, 419-422, 1991
A:Title: Polymorphism of the human gamma chain fibrinogen gene.
A:Reference number: I37390; MUID:92119334
A:Accession: I37390
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 75-286 <RES>
A:Cross-references: EMBL:X51473; NID:g931410; PIDN:CA535837.1; PID:g930064
C:Comment: The two forms of gamma chain, A (see PIR:FGHUG) and B, arise by alternative splicing, which makes this chain different from the gamma-B chain at positions 434-437 and
C:Comment: The gamma-B chain is present in about 10% of the fibrinogen molecules in plasmas.
C:Genetics:
A:Gene: GDB:FGC
A:Cross-references: GDB:119132; OMIM:134850
A:Map position: 4q28-4q28
A:Introns: 26/3; 41/3; 103/2; 134/2; 178/1; 222/3; 284/2; 377/1
C:Complex: The fibrinogen molecule is a hexamer containing two sets of alpha (see PIR:FGHUG) and beta chains. The alpha chains are contained in the core. Two three-chain coiled coils emerge from this core and connect to the distal domain nodes.
C:Function:

```

A:Description: fibrinogen cleaved by thrombin yields monomers that are polymerized in  
A:Pathway: blood coagulation  
C:Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology  
C:Keywords: alternative splicing; blood coagulation; calcium; coiled coil; glycoprote  
F:1-26/Domain: signal sequence #status predicted <Sig>  
F:27-43/Product: fibrinogen gamma-B chain #status experimental <MP1>  
F:116-415/Domain: fibrinogen beta/gamma homology <PRG>  
F:341-355/Domain: calcium binding #status predicted <CAB>  
F:400-422/Region: polymerization site; binding to the amino end of the alpha chain of  
F:34/Dissulfide bonds: interchain (to gamma-35) #status predicted  
F:35/Dissulfide bonds: interchain (to gamma-34) #status predicted  
F:45/Dissulfide bonds: interchain (to beta-110) #status predicted  
F:49/Dissulfide bonds: interchain (to alpha-64) #status predicted  
F:78/Binding site: carbohydrate (asn) (covalent) #status predicted  
F:161/Dissulfide bonds: interchain (to beta-227) #status predicted  
F:165/Dissulfide bonds: interchain (to alpha-180) #status predicted  
F:119-208 352-365/Dissulfide bonds: #status predicted  
F:424/Cross-link: isopeptide (Gln) (interchain to Lys-432 N6-amino) #status predicted  
F:433/Cross-link: isopeptide (Lys) (interchain to Gln-424) #status predicted

```
Query Match          17.7%; Score 371.5; DB 1; Length 453;
Best Local Similarity 31.9%; Pred. No. 1.8e-21;
Matches 105; Conservative 42; Mismatches 129; Indels 53; Gaps 11;

QY      NSIYSVTRSTKKLLRNMMDEQ-----CASDYLSNQVNEMLNRVLITTFEVRKOLDPF 138
       | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      NMIDAATLAKSKMEEIKRYEASILTHDSSIRLYDETINSNOKIVNLKEV--AQLEAQ 160

QY      139 PHRP---VQSHPH---GLDCDTDKIDTIGSVTKPGAGLIYIHPEGSSYPPEVMCDNDYRGCG 191
       | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      161 CQEPCCKDVVQLHDITGKDCOD----IANKGAKGSGLVFIFPKLANOQFLVYCEIDSGNG 216

QY      192 WTVYQKRITDIILDRQLMCVDLDGFGLD---LGEFWLGKLKITTYLNQKRTSMLYAL 247
       | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      217 WTVYQKRDLGVSDERKKNMIQYKEEGFHLSPGTTEFWGNKRILHTISQAIPALRVEL 276

QY      248 ESEDDTLAAVSAYDNFNWLEDETRPFKMHGRYS-GNAGDAFGLAKED-----NONAM 298
       | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      277 EDWMGRISTADYIAEFKVGPENDKTRLTYATFRAGGDAGAFGFGDDPSDKFTSHGM 336

QY      299 PFSTDVDNDNCRCRPACTLVNGSVKSCSHLNKTKTWFMFNECCLANIIGHFSCKL----- 353
       ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      337 QFSTWMDNNNDKFEGNCARQDGS-----GWMMNKCHAGHLNCGYYGGGYSKAST 385

QY      354 ---LATGIQWGTWKNSPVKIKSVSMKI 379
       || |||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      386 PNGYDNGIIIMATW--KTRWYSMKKTMTKI 412

RESULT    9
fibrinogen beta chain - chicken (Fragment)
C:Species: Gallus gallus (chicken)
C>Date: 31-Jul-1991 #sequence_rev1sion 31-Jul-1991 #text_change 13-Aug-1999
C:Accession: A38463
R:Weissbach, L.; Oddoux, C.; Procyk, R.; Grieninger, G.
Biochemistry 30, 3290-3294, 1991
A>Title: The beta chain of chicken fibrinogen contains an atypical thrombin cleavage
      Reference number: A38463; MUID:91182745
A:Accession: A38463
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-463 <WEI>
A:Cross-references: GB:A58514; NID:g211779; PIDN:AAA48770.1; PID:g211780
C:Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen dsu
F:73-202/Domain: fibrinogen disulfide ring homology <PDR>
F:212-460/Domain: fibrinogen beta/gamma homology <FBG>

Query Match          17.7%; Score 371.5; DB 2; Length 463;
Best Local Similarity 27.7%; Pred. No. 1.8e-21;
Matches 112; Conservative 57; Mismatches 136; Indels 99; Gaps 17;
```

```

Oy  94  TKLLRNMDQASLDYLSNQVNELMNRKLLLTTEVFQKDRPRNRPVOSHGDCTDI 153
      | : : : : : | : : : : : | : : : : : | : : : : : |
Db  189  MKSVLEHRAKMQMEBAITQ - KCLCSAPCTNCRV -----PVVS-GMNCEDI 235
      | : : : : : | : : : : : | : : : : : | : : : : : |
Oy  154  KDTIGSVTKPRPSGLYIINRGSSVPEVMDMDYRGSGVTIQRKIDGIDRQLMYCYL 213
      | : : : : : | : : : : : | : : : : : | : : : : : |
Db  236  YRNGRTSEA---YIQRDIFSPRYVFECDMSHGSGMTVVOONRVDGSSNFAKRMNTYK 291
      | : : : : : | : : : : : | : : : : : | : : : : : |
Oy  214  DGFDDL-----GEFMILGKKIFIVNQKMTSEMLVVALESEDDTLAVASYDNF 262
      | : : : : : | : : : : : | : : : : : | : : : : : |
Db  292  AEFNGINAGNCKSTCINPGEYWTGKTIVQDLTQ -HTQOVLFDMSMBESSV-YAQTASF 349
      | : : : : : | : : : : : | : : : : : | : : : : : |
Oy  263  WLEDETRFFKMHILGRYSGNAGDA -FRQLK - -EDNO-----NAMPSTSDVNDCCRPAC 314
      | : : : : : | : : : : : | : : : : : | : : : : : |
Db  350  RPEMDAGYRLWVEDYDSGNAGNMLBEGATQMDMDNTWTIINGMGSTFDRDNDWNP - - 407
      | : : : : : | : : : : : | : : : : : | : : : : : |
Oy  315  LVNGQSVKSCSHLHNKTGMFNEBSCGANLNGIHNSG---KLA-----TG1QMGTTWKN 366
      | : : : : : | : : : : : | : : : : : | : : : : : |
Db  408  ---GDPRHCSR -EDAGGMWYNRCHANPRGRYVGMGIYTKQADYGTDDGVVMNMW--K 461
      | : : : : : | : : : : : | : : : : : | : : : : : |
Oy  367  NSPYKIKSVSMKIR 380
      | : : : : : | : : : : : | : : : : : | : : : : : |
Db  462  GSWYSMRQMAKKIR 475

RESULT 11
505313
fibrinogen gamma-B chain precursor - bovine

```

RESULT 11  
S05313  
fibrinogen gamma-B chain precursor - bovine  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 07-Sep-1990 #sequence.revision 07-Sep-1990 #text\_change 13-Aug-1999  
C:Accession: S05313  
R:Brown, W.M.; Dziegielewska, K.M.; Foreman, R.C.; Saunders, N.R.  
Nucleic Acids Res. 17, 6397, 1989  
A:Title: Nucleotide and deduced amino acid sequence of a gamma subunit of bovine fibr  
A:Reference number: S05313; MUID:89366676  
A:Accession: S05313  
A:Molecule type: mRNA  
A:Residues: 1-444 <BR>  
A:Cross-references: EMBL:X15556; NID:q349; PIDN:CA333662.1; PID:q350  
A:Note: the authors translated the codon AGT for residue 105 as Ala and ATT for resid  
C:Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology  
F1-24/Domains: signal sequence #status predicted <Sig>  
F1-25-444/Product: fibrinogen gamma-B chain #status predicted <MAT>  
F174-414/Domains: fibrinogen beta/gamma homology <FBG>

	Query Match	17.3%	Score 365;	DB 2;	Length 444;
	Best Local Similarity	30.2%	Pred. No. 5,6e-21;		
	Matches 100;	Conservative	51;	Mismatches 124;	Indels 56; Gaps 12.
QY	85 NSIVSYTRSTKTLKLNMM-----DEQAQSLDLYLSNQVNELNNRYLLTTEVERKQLDPF	138			
	101 NIIESATKNKSMMEIMKIELTIISTHETINFLEGVNSQKILVNLDKYV--QLKAN	158			
QY	139 PRRPVQS-----HGLDCTDIKDTIGSYATKPRSGLYIIHPGSSYPEEVMCDMDYRGCG	191			
DB	159 COEPCQDVTYKIDHYVGRDCQD---VANKAGESGLYETFRPL-KAKQFLVYCEIDSGSGNG	213			
QY	192 WTVIICKRIDGIIIDPQRLMDYLDYDFGDDL-----GEPLGLSKTKFYIYNOKNTSPMLY	245			
DB	214 WTVFQKRLDGSIDPEKKNWLYQVEKGCHLSPTGTGNTETFLVGEKHIHLISTOSSIPVLKI	273			
QY	246 ALESEDDTLAIVASYNFWLEDETFREFKMLIGRY-SGNADADRGLKKED-----NNN	296			

```

Db      274  QLEDMNGRSTADYASFSVYTGENDRRLTYLAFYFGGDGADFAFDGYDGDGDSDDFFFTSHN 336
Oy      297  AMPEFTSVYDNDGCGPACPLATVNGOSVSCSHLNKTKMFMNFCGLANLGNHFEFGKLLAT 358
        ||||| ||| |
Db      334  GMGFTSDMDNDKRYDNGC---AEQY-----GIGMMNKNCHAGHLNGVYVQGGTYSKT 382
Oy      357  -----GIQMGFTWTKNNSPVRIKLSVSKI 379
        ||||| : |||

```







Best Local Similarity	36.8%;	Pred. NO. 4.4e-20;			
Matches	92; Conservative	31; Mismatches	96; Indels	31; Gaps	10;

[illegible]

RESULT 15

scabrous locus (sca) protein precursor - fruit fly (*Drosophila melanogaster*)  
C:Species: *Drosophila melanogaster*  
C:Date: 31-Jan-1992 #sequence\_revision 31-Jan-1992 #text\_change 01-Dec-2000  
C:Accession: A39832; S58998  
R:Baker, N.E.; Mlodzik, M.; Rubin, G.M.  
A:Title: Spacing differentiation in the developing *Drosophila* eye: a fibrinogen-related  
A:Reference number: A39832; MUID:91075223  
A:Accession: A39832  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-774 <BAK>  
A:Cross-references: GB:M60065; GB:M37703; NID:q158401; PID:q158402  
R:Hu, X.; Lee, E.C.; Baker, N.E.  
A:Title: Molecular analysis of scabrous mutant alleles from *Drosophila melanogaster* indi  
A:Reference number: S58998; MUID:96109607  
A:Accession: S58998  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-18, 'T', 20-774 <HDX>  
C:Genetics:  
A:Gene: FlyBase:sca  
C:Cross-references: FlyBase:FBgn0003326  
A:Superfamily: fibrinogen beta/gamma homology  
F:514-711/Domain: fibrinogen beta/gamma homology <FBG>

Query Match	16.6%;	Score 348.5;	DB 2;	Length 774;
Best Local Similarity	25.1%;	Pred. No. 2.3e-19;		
Matches 100; Conservative	65;	Mismatches 137;	Indels 97;	Gaps 14

[illegible][illegible]

Search completed: May 22, 2002, 15:08:30  
Job time: 197 sec

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94 ---TKKLLRNMDEQASL-----DYLSNQVN--ELMNRVLLLTTEVERFKQL 135

```

Db 353 EAMFTSTYTHAVEYQPKVITSESGVNIROCVATNETEGIEFTSRILRAT----- 404
QY 136 DPPRHPVOSHGL--DCTDIKDTIGSVYTPPSGLYIIHEGSSYPPEVWCMDDYRGSGMT 193
Db 405 NPTPYVDGCTESLPYDCAEELY-----ARGVROSGSVYDIRP-GTKVMTYVCCMDMTDGGGWT 459
QY 194 VIOKRIDGIIDQRLMCDYLDGFGDLGFEWLGKIKFIYI-VNOKRTSMFLYALESEDD 252
Db 460 MIOQRIDGIIVNSKSKGSKSTKNGFDINADHWIGLEKMHHSITSNKSRRMELRLINTDWD 519
QY 253 TLAYASIDNFWLEDETRPFKMLGRYSGNADAFRLKKEDNONAMPFSTSDVNDGCRP 312
Db 520 VSHYANAYGVFRIRSECKNVQLAKRTYGTAGDAL-NYGENYNHHLQPTTFEDRDND----- 574
QY 313 ACLVNGQSVKSCSHLNTKGMFNECCGLANLNGIHHSFG--KLATGIOMGTWTK----- 365
Db 575 -----GYALNGCGRYR-RSGWFMNACFANLNG-NYTTGPKYGVONGIYWGTYKRLSDST 627
QY 366 NNSPVYKIKSVSMKIR 380
Db 628 SNSRYSFKYDMKVR 642

```

## RESULT 2

```

ID 095841 PRELIMINARY: PRT: 491 AA.
AC 095841:

```

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DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE ANGIOPOIETIN Y1 (D0595C2.2) (ANGIOPOIETIN-RELATED PROTEIN 1
DE PRECURSOR)
GN D0595C2.2 OR ARPL
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN 11
RP SEQUENCE FROM N.A.
RC TISSUE=HEART;
RX MEDLINE=99148829; PubMed=10025962;
RA Kim I., Kwak H.J., Ahn J.E., So J.N., Liu M., Koh K.N., Koh G.Y.;
RT "Molecular cloning and characterization of a novel angiotensin family
RT protein, angiotensin-3."
RL FEBS Lett. 443:353-356(1999).
RN 12
RP SEQUENCE FROM N.A.
RA Cobley V.;
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
RN 13
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RA Ota T., Nishikawa T., Kawai Y., Suzuki Y., Ishii S., Saito K.,
RA Yamamoto J., Sugano S., Isogai T.;
RT "HRI human cDNA sequencing project."
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN 14
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RA Ito Y., Oike Y., Yasunaga K., Matsumoto S., Ota T., Nishikawa T.,
RA Kawai Y., Isogai T., Hamada K., Saito Y., Miyata K., Masuno Y.,
RA Suda T.;
RT "Molecular cloning and characterization of novel angiotensin-related
RT protein (ARp4)."
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF107253; AAD19608.1; -
DR EMBL: AL355520; CAC13169.1; -
DR EMBL: AB056476; BAB40691.1; -
DR HSSP: P02671; 1FZD.
DR InterPro: IPR002181; Fibrinogen_C.
DR Pfam: PF00147; fibrinogen_C; 1.
DR SMART: SM00186; FBG; 1.
DR PROSITE: PS00514; FIBRIN_AG_C_DOMAIN; 1.

```

```

KW Signal. 1 23
FT SIGNAL. 24 491 POTENTIAL.
FT CHAIN. 24 491 POTENTIAL.
SQ SEQUENCE 491 AA: 56719 MW: 3C4DB8DEFCE7E99 CRC64:

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Query Match 20.2%; Score 425; DB 4; Length 491;
Best Local Similarity 26.9%; Pred. No. 1e-27;
Matches 119; Conservative 64; Mismatches 133; Indels 126; Gaps 14;

```

```

QY 44 SNAKDESKNDYVCKEDCEECQVKTITRE-EKHMCNCLNSTYVSRSTKLLRNKM 102
Db 68 TKQGDASTIKDMMTRDLENLADYLSRQKREIDVLDLVVDGQVNYEVKLLRKESRNN 127
QY 103 DE-QQASLDYL-----SNQVELMNRVLLTTE----- 129
Db 128 SRVTQLYQMLHEIIRKRDNSLELSQENKILNTVTEMLKMATRYELEVKYASLTDLVN 187
QY 130 -----VFRQO---LDP-----PDRPVOSHGL----- 148
Db 188 NOSVMITLLEEOQLRIFSRQDTHVSPPLVQVPHLPNSQOYTPGLGNETIORPGYPR 247
QY 149 DCTDIKDTIGSVYTKRP-----SGLYTHPGSSYPFEV 181
Db 248 DLMRPEDLATSPKSPFKIPVTFINEGPFKCCQAKKENGHSVGLTLMKPENSGNPMOL 307
QY 182 MCDMDYRGSGWTVIOKRIDGIIDFORLWCDYLDGFGDLGFEWLGKIKFIYVNOKNTSF 241
Db 308 WENSIDPDCGWTYIOKRTDGSVNFPMENYKKGFCGNDGEYWLGENIYMLSNQDN--Y 365
QY 242 MLYVALESDDPLAYSYNFMLEDETRPFKMLGRYSNADAFRLKKEDNONAMPSS 301
Db 366 KLTELEWSDKRVYAEVSSFRLEPSEFYLRLGLYQGNADSDMMW-----HNGKQFT 419
QY 302 TSDVDNDGCRPACLVNGQSVKSCSHLNTKGMFNECCGLANLNGIHHSFGKLLA--TGI 358
Db 420 TIDRDKD-----WAGNCANRH-KGWMYVNCANSLNGLVYRGCHIRSKHDOI 468
QY 359 QWGTWTKNNSPVYKIKSVSMKIR 380
Db 469 FMAEY--RCGSYSLRVQCMIR 488

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## RESULT 3

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ID 09EP77 PRELIMINARY: PRT: 357 AA.
AC 09EP77:

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DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE PROTHROMBINASE FGL2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RA Rychlik D.F., Chien E., Philippe M.;
RT "FGA2 Expression in the Sprague-Dawley Rat."
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF323608; AAG42269.1; -
DR HSSP: P02671; 1FZD.
DR InterPro: IPR002181; Fibrinogen_C.
DR Pfam: PF00147; fibrinogen_C; 1.
DR SMART: SM00186; FBG; 1.
DR PROSITE: PS00514; FIBRIN_AG_C_DOMAIN; 1.
SQ SEQUENCE 357 AA: 40966 MW: 31183DD9A02EBBA9 CRC64:

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Query Match 19.5%; Score 409.5; DB 11; Length 357;
Best Local Similarity 32.0%; Pred. No. 1.4e-26;
Matches 121; Conservative 50; Mismatches 150; Indels 57; Gaps 15;

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QY 36 VVNIIVEDGSNAKDESKSNDYVCKEDCESCDV--KTKITREKHFMCNLSIVSYTRS 93
Db 4 VLKEKRIQLQEAVIDSLKSCQDCKLQADHPDPCGNGAFTAD-----NRVOELSESQVNK 57
QY 94 TKKLRLNMDEBOQA-----SL-----DLSNQVNEIMNRLTLTTEVFR----- 132
Db 58 LSSEKNAKKEELIQLQGLQLESLQLVNMNNIENYDNKAVANLTSVNSLDSCKFKPCSGE 117
QY 133 KOLDFPFRPVQSHGLDCTIDKDTIGSYTKTPSGLYIHPGSSYFPEVWCDMDYRGCGW 192
Db 118 NQPNPVOHLIKY----DCSDYY-VLG---KRSSGTYRVPDPHRNSSEFYVCDMETTGCGW 169
QY 193 TVICKRIGIIDFQRLMCDYLDGFGDLGFEFMLGLKTFEYVONKNTSPFMYLVLESDD 252
Db 170 TVLDARLDGSTNFTRGKMDYKAGFENLEREFWLGNDKTHLIT--KSKEMILRLIDLEDPNG 227
QY 253 TLAAVASYDNFWLEDETRFKNHGLRGYSQMGADAFRGLKEDNONAMPSTSDVDNDGCRP 312
Db 228 LTLVAAYDQFVAVNEFLKYLRLHGLNYNGTAGDALR-FSRHYNHDLRFFTPDRODRYPS 286
QY 313 ACLVNGOSVSKCSHLHNTGWMFNECGLANLNGIHH--FSGKLATIGQGTW--TKNN 367
Db 287 G-----KCG-LYSSSGWMFACLSANLNGKYNOGRYG--VRNGIFWGTPGVGSOA 334
QY 368 SPVKIKSYSMKIRRMYNP 385
Db 335 HPGGYKESFEKAKMKMIRP 352

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## RESULT 4

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Q9J03 PRELIMINARY: PRT: 493 AA.
ID 09J03; AC 09J03; DT 01-OCT-2000 (Tremblrel, 15, Created)
DT 01-OCT-2000 (Tremblrel, 15, Last sequence update)
DT 01-DEC-2001 (Tremblrel, 19, Last annotation update)
DE ANGIORENSIN II TYPE 1A RECEPTOR ASSOCIATED PROTEIN.
OS Rattus norvegicus (Rat). Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
CX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MSTAR-KYOTO. TISSUE=VASCULAR SMOOTH MUSCLE;
RA Guo D.F., Baranes D., Ono Y., Porter J.P., Abl-Jacode E., Orlov S.N.,
RT Inagami T.;
RT "ARAP1 is required for recycling and reensensitization of angiotensin II
type 1A receptor."
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF159049; AAF80364.1;
DR HSSP: P02671; IZFD.
DR InterPro: IPR002181; Fibrinogen_C.
DR Pfam: PF00147; Fibrinogen_C.1.
DR SMART: SM00186; FBG.1.
DR PROSITE: PS00514; FIBRIN_AG_C_DOMAIN.1.
KW Receptor.
SQ SEQUENCE 493 AA; 57159 MW; 7C37652C472B2341 CRC64;

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Query Match 19.2%; Score 404.5; DB 11; Length 493;
Best Local Similarity 27.1%; Pred. No. 5.6e-26;
Matches 108; Conservative 68; Mismatches 118; Indels 105; Gaps 15;
QY 62 EESCDVTKIT-----REEKHFMCNLSIVSYSTRSKLLRNMDQO--A 107
Db 125 KESRMNRSRVOLYQMLHEIIRKRDNALESOLEIRILNOTADMLQVSKYKDEHFKQ 184
QY 108 SLDIYSNOVNEIM-----NRVL--LITTEVR 132
Db 185 HLDMLAHQSEVIAQLAEHCORVAPARVPDPAPPTPRVYQPPYNNRIINOISTNEIOS 244
QY 133 KO---LDP-FPHRPVOSHGLDCTIDKDTIGSVTKTPSG-----LYII 170

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Db 245 DQNLKVLPSPLTPEAL-----SLPSSIDKPEGPRDCLQALEDSHTSSITLV 294
QY 171 HPESSSYFEEVWCDMDYRGCGWTVIQRKIDIIDFQRLMCDYLDGFGDLGFEFMLGLKTI 230
Db 295 KPEMTNRLMQVACDQHRHDPGCVTVIQRDLDSVNEFRMVEYTKQGFNGIDEEWLGLENI 354
QY 231 FYIYNQKTSFMLVALESEDDTLAAYSDYDNFWLEDEFRTFKMLGRSGNAGDAFRGLK 290
Db 355 YWLTNQN--YKLLVTYMDWSGRVFAFYASFRLPESEYTKLRGRHGNAGSFTW-- 410
QY 291 KEDNONAMPSTSDVDNDGCRPACILVNGOSVSKCSHLHNTGWMFNECGLANLNGIHFS 350
Db 411 -----HNGKQFTLDRDH-----YVIG-----NCAH-YQKGGWYVNCASHNLNGVWYRG 455
QY 351 GKLLA---TGIQWGTWTKNNSPVKIKSYSMKIRRMYNP 386
Db 456 GHYRSRYQDGYVMAEF--RGGSYSILKRYVMIRPNPNF 492

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## RESULT 5

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Q90218 PRELIMINARY: PRT: 489 AA.
ID Q90218; AC Q90218; DT 01-DEC-2001 (Tremblrel, 19, Created)
DT 01-DEC-2001 (Tremblrel, 19, Last sequence update)
DT 01-DEC-2001 (Tremblrel, 19, Last annotation update)
DE ANGIOPOIETIN-2.
GN ANG2.
OS Brachydanio rerio (zebrafish) (zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Danio.
CX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21391693; PubMed=11500985;
RA Pham V.N., Roman B.L., Weinstein B.M.;
RT "Isolation and expression analysis of three zebrafish angiotensin
genes."
RL Dev. Dyn. 221:470-474(2001).
DR EMBL: AF379603; AAK83348.1;
SQ SEQUENCE 489 AA; 55785 MW; 3ABAE6278539B33C CRC64;

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Query Match 19.0%; Score 399.5; DB 13; Length 489;
Best Local Similarity 28.1%; Pred. No. 1.5e-25;
Matches 114; Conservative 55; Mismatches 131; Indels 105; Gaps 16;

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QY 23 VQGNCVHHSSTDSVVNIIVEDGSNAKDESKSNDYVCKEDCESCDVTKITREKHFMCRN 82
Db 107 MERNVIHTQT-----ATMLEIGTNLISQSAEN--TCK-----LTDEYVQLNQT-----R 150
QY 83 LQNSIVSYSTRSKLLRNMD-----EQQA 107
Db 151 LEIQLEYSLSSTNRLERKQLLBQTOEVSRLDNKNSYMEGRFADMEAKHSRELQAIQEQKQ 210
QY 108 SLDIYSNOVNEIM-----RVLLITTEVRKQOLDPPH-----RPVQS 145
Db 211 LLELDLRO-NELVSLLEGEELASSTRNSTLIQROQASLDTVQOQLAMVTHCNDISTPVDK 269
QY 146 HGL--DCTDI-KDTIGSVTKTPSGLYIHPGSSYFPEVWCDMDYRGCGWTVIQRKIDG 201
Db 270 EMLKFRDCAELFKSGV-----TENGISILHPNSTQKIKVCIDMKTKGGWTVIQHRYDG 324
QY 202 IIDFQRLMCDYLDGFGDLGFEFMLGLKTFIYNQKNTSPFMYLVLESDDTLAAYASYDN 261
Db 325 SVDFNRMDNDYKLGFGDPSGHEWLGNDVIHLTTTKD--YTLQVHLKDAEHHQAYSQYDT 382
QY 262 FWLEDETRFKNHGLRGYSQMGADAFRGLKEDNONAMPSTSDVDNDGCRPACLVNGOSV 321
Db 383 FYIDEDKRYSLHAKGFSGTAGRT-----SSLTJHSGTQFSTRKDDNDQC----- 426

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OY 322 KSCSHLHNT-GWMEGCLANLNGIHNF--SGKLATGICGWTW 363  
DB 427 -SCKCAQMATGGMWPEACGSPNLNGIYSGNSNIVRYSIKWY 470

RESULT 6  
008830 PRELIMINARY: PRT: 312 AA.

AC 008830:  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE HYPOPHNETICAL 36.4 KDA PROTEIN PRECURSOR.  
GN HRP-1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=LIVER;  
RX MEDLINE=93290661; PubMed=8390249;  
RA Yamamoto T., Gotoh M., Sasaki H., Terada M., Kitajima M.,  
Hirohashi S.;  
RT "Molecular cloning and initial characterization of a novel fibrinogen-  
related gene, HRP-1".  
RL Blochem. Biophys. Res. Commun. 193:681-687(1993).  
DR EMBL: D14446; BAA03336.1; -.  
DR HSP: P02671; IPI2D.  
DR InterPro: IPR002181; Fibrinogen\_C.  
DR Pfam: PF00147; fibrinogen\_C; 1.  
DR SMART: SM00186; FBG; 1.  
DR PROSITE: PS00514; FIBRIN\_AG\_C\_DOMAIN; 1.  
KW Signal; Hypothetical protein.  
FT SIGNAL 1 17 POTENTIAL.  
FT CHAIN 18 312 UNKNOWN PROTEIN.  
SQ SEQUENCE 312 AA: 36378 MW: 2330F3D60CDD0BBA8 CRC64;

Query Match 18.9%; Score 397; DB 4; Length 312;  
Best Local Similarity 34.3%; Pred. No. 1.3e-25;  
Matches 111; Conservative 44; Mismatches 115; Indels 54; Gaps 12;

OY 87 IYSYRSTKLLRNMDDEQASLDYLSNOVNLNRYLLTTEVRKQ----- 134  
DB 4 VSEFLVLTAL--MGRISALEDCAOEMRLRAOVRLLETRVKKQOVKIKQLDENEV 60  
OY 135 --LDPEFHRPVQSHG-----LDCTDIKDTIGSVTKTPSGLYIIHREGSSYPREVMCDMDY 187  
DB 61 QFLDKGDEPTVVDLSKROYADSCSEIFNDGYKL-----SGFYKIKPLQSPAESVYCDMS- 115  
OY 188 RGGGWTVIQKRIDGIIDFQRLWC DYLDGFGDLL--GEFWLGKIKFYLVNKNKTSFMYL 244  
DB 116 DCGGWTVIQKRSDGSENFNRGKDYENGFGNFVQKHGEWLGKKNLHFLTQED--YTLK 173  
OY 245 VALSEDDTLAASVDNFELEDETRFEKMHILGRYSGNAGDAFRGLKEDNQ-----NAMP 299  
DB 174 IDLADFENKSRAYQKKNFVGDEKNEFYLEINIGESTAGDSLAGNHPNPOWMAASHORMK 233  
OY 300 FSTSDVNDGCRPACLVNGQSVKCSHLNKNKGWMEGCLANLNGIHFGSKLLA---T 356  
DB 234 FSTWBRDHNHYGNCNCAEEQS-----GWMFNCHSANLNGV-YISGPTYAKTDN 281

RESULT 7  
O96KM6 PRELIMINARY: PRT: 312 AA.  
ID O96KM6:  
AC O96KM6:  
DT 01-DEC-2001 (TREMBLrel. 19, Created)

DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE HP-041.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=LIVER;  
RX MEDLINE=21363035; PubMed=11470158;  
RA Hara H., Yoshimura H., Uchida S., Toyoda Y., Aoki M., Sakai Y.,  
Morimoto S., Shiohara K.;  
RT "Molecular cloning and functional expression analysis of a cDNA for  
human heparosucin, a liver-specific protein with hepatocyte mitogenic  
activity".  
RL Blochim. Biophys. Acta 1520:45-53(2001).  
DR EMBL: D87342; BAB70690.1; -.  
SQ SEQUENCE 312 AA: 36407 MW: 0E281F4646FB34CC CRC64;

Query Match 18.9%; Score 397; DB 4; Length 312;  
Best Local Similarity 34.3%; Pred. No. 1.3e-25;  
Matches 111; Conservative 44; Mismatches 115; Indels 54; Gaps 12;

OY 87 IYSYRSTKLLRNMDDEQASLDYLSNOVNLNRYLLTTEVRKQ----- 134  
DB 4 VSEFLVLTAL--MGRISALEDCAOEMRLRAOVRLLETRVKKQOVKIKQLDENEV 60  
OY 135 --LDPEFHRPVQSHG-----LDCTDIKDTIGSVTKTPSGLYIIHREGSSYPREVMCDMDY 187  
DB 61 QFLDKGDEPTVVDLSKROYADSCSEIFNDGYKL-----SGFYKIKPLQSPAESVYCDMS- 115  
OY 188 RGGGWTVIQKRIDGIIDFQRLWC DYLDGFGDLL--GEFWLGKIKFYLVNKNKTSFMYL 244  
DB 116 DCGGWTVIQKRSDGSENFNRGKDYENGFGNFVQKHGEWLGKKNLHFLTQED--YTLK 173  
OY 245 VALSEDDTLAASVDNFELEDETRFEKMHILGRYSGNAGDAFRGLKEDNQ-----NAMP 299  
DB 174 IDLADFENKSRAYQKKNFVGDEKNEFYLEINIGESTAGDSLAGNHPNPOWMAASHORMK 233  
OY 300 FSTSDVNDGCRPACLVNGQSVKCSHLNKNKGWMEGCLANLNGIHFGSKLLA---T 356  
DB 234 FSTWBRDHNHYGNCNCAEEQS-----GWMFNCHSANLNGV-YISGPTYAKTDN 281

RESULT 8  
O96OM6 PRELIMINARY: PRT: 312 AA.  
ID O96OM6:  
AC O96OM6:  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE UNKNOWN (PROTEIN FOR MGC:12455).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=LIVER;  
RA Struhsberg R.;  
RL Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: BC007047; AA07047.1; -.  
SQ SEQUENCE 312 AA: 36379 MW: 9297J53AEA746C31 CRC64;

Query Match 18.8%; Score 396.5; DB 4; Length 312;  
Best Local Similarity 35.0%; Pred. No. 1.5e-25;

ID	Q9BDY8	PRELIMINARY;	PRT;	498 AA.
Q9BDY8				
AC	Q9BDY8;			
DT	01-JUN-2001 (TREMblrel, 17, Created)			
DT	01-JUN-2001 (TREMblrel, 17, Last sequence update)			
DT	01-DEC-2001 (TREMblrel, 19, Last annotation update)			
DE	ANGIOPOIETIN 1.			
OS	Sus scrofa (Pig).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.			
OX	NCBI_TaxID=9823;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=1153163; PubMed=11230987;			
RA	Kim I., Moon S.O., Han C.Y., Pak Y.K., Moon S.K., Kim J.J., Koh G.Y.;			
RT	"The angiotensin-II $\alpha$ 2 system in coronary artery endothelium prevents			
RL	oxidized low-density lipoprotein-induced apoptosis.";			
DR	Cardiovasc. Res. 49:872-881(2001).			
DR	EMBL; AF233227; AAK14992.1; -			
DR	HSSP; P02671; 1FZD.			
DR	InterPro: IPR002181; Fibrinogen_C.			
DR	Pfam; PF00147; fibrinogen_C; 1.			
DR	SMART; SM00186; FBG; 1.			
DR	PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.			
SO	SEQUENCE 498 AA; 57413 MW; A8C1C8EF556061876 CRC64;			

[illegible]

RESULT	ID	PRELIMINARY:	PRT:	308 AA.
AC	Q908W6			
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DE	01-JUN-2001 (TREMBLrel. 17, Last annotation update)			
OS	TECHYLECTIN-5B ISOFORM.			
CC	Tachyleus tridentatus (Japanese horseshoe crab).			
CC	Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;			
OX	NCBI_TaxID=6853;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=99398666; PubMed=10468566;			
RA	Gokuden S., Mita T., Tsuda R., Koori K., Kawahara T., Seki N.,			
RA	Mizuno Y., Wai S.N., Iwanaga S., Kawahara S.;			
RT	"Horseshoe crab acetyl group-recognizing lectins involved in innate			
RT	immunity are structurally related to fibrinogen.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 96:10086-10091(1999).			
DR	EMBL; AB024739; BAB84190.1; -			
DR	HSSP; P02671.1F2D.			
DR	InterPro; IPR002181; Fibrinogen_C.			
DR	Pfam; PF00147; fibrinogen_C.1.			
DR	SMART; SM00186; FBC.1.			
DR	PROSITE; PS00514; FIBRIN_AG_C.DOMAIN.1.			
SO	SEQUENCE 308 AA; 35156 MW; 36161655E77E0BF CRC64;			

Query Match	18.28;	Score 363.5;	DB 5;	Length 308;
Best Local Similarity	29.58;	Pred. No. 1.8e-24;		
Matches 114;	Conservative 45;	Mismatches 116;	Indels 111;	Gaps 15;
QY	1	LFLANVCIFCGEYVQNCVHH-----STPSSVYNIYEDGSSNKADESKSDYCKEDCEES	64	
DB	8	LSFLVCSLIVAGG-----VHHHAACTYCSLKGILIDVSDDLTLAKER-----	50	
QY	65	CDVKTKITREEKHEFKMCRNLQNSIVSYTRSTKLLRRMMEDQOASLDYLSNOVNELMNRVL	124	
DB	51	-----LATLQNSICSDKAF-----YMETYNIVNQK--	77	
QY	125	LITTEVEFRKQLDPEPHRPVQSHGL--DCFDIKDTIGSVKTPDSGLYIHPDESSYPFEEYM	182	
DB	78	-----AEKNGLPINCIA---TYVQCGNFRISGIMYIMPLFLNHPISVF	115	
QY	183	CDMDYRGCGMTYIQRIKID---GLIDPQRLMCDYLDSEFGDLGEEFWGLKIFIVYNQKMT	239	
DB	116	CDMETAGGGMTYIQRGDGGQPIQNFQYQWESKKNFGMLTKFEWFGANDIIFVLNQ--D	173	
QY	240	SFMLYALASEDDTLYVASYDNFMLEDETFRPFMHJGGRYSGNAGDAFRGLKEDKEDNONAMP	299	
DB	174	SVYLRRDLEDFEGCGRRYAEVEFLVASELELYIMASKYTKGDAQDSL-----SCHNNMP	227	
QY	300	FSTSDVDNDCGRCFACLVNGQSVKCSHLHNKGTGWMEFNECGLANLNCI-----HHFSGKLL	354	

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Db 228 FTTKDRDND-----KKEKNCAEAY-KGGWYNACHSHNLNGMTLRGPHES----- 272
Qy 355 ATGIQWGTWTKNNSPVKIKSYSMKIR 380
Db 273 AVGVNMYQWRGHNYSLKVS--EMKIR 296

RESULT 11
Q9P2Y7 PRELIMINARY; PRT; 495 AA.
AC Q9P2Y7
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE ANGIOPOIETIN-2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99126459; Pubmed=9927494;
RA Tanaka S., Mori M., Sakamoto Y., Makuuchi M., Sugimachi K.,
RA Manda J.R.,
RT "Biologic significance of angiotensin-2 expression in human
RT hepatocellular carcinoma.";
RL J. Clin. Invest. 103:341-345(1999).
DR EMBL; AB009865; BAA95590.1; -.
DR HSSP; P02671.1F2D.
DR InterPro; IPR002181; Fibrinogen_C.
DR Pfam; PF00147; fibrinogen_C; 1.
DR SMART; SM00186; FBG; 1.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
SQ SEQUENCE 495 AA; 56848 MW; EBFAC35ABF1F08F6 CRC64;

Query Match 18.2%; Score 382; DB 4; Length 495;
Best Local Similarity 26.4%; Pred. NO. 4.5e-24;
Matches 110; Conservative 73; Mismatches 138; Indels 96; Gaps 16;

Qy 23 VQGNVHSTSSVYNIVEDGSNAKDESKNDTVCKEDCESCDVTKIT---TREE--- 75
Db 112 IQQNAVQNOT---AVMEIGTNLNOT-----AEOTRLTDEAVOYLANOTTRLEQL 160
Qy 76 -KHFRCRN-LQNSIVSYSTRSKL-----LRNMDEQOASL 109
Db 161 LEHSLSTKKLEKQILDQTSINKLQDKNSPLEKKVLAEMDKHIIQLQSIKEKQDQLVLY 220
Qy 110 DYLSNQVVELNRYLLN--TEVERKQ-----LDPPRHRYQSHG 147
Db 221 SKQNSIIELEKKIYATATVNSVLDKQOHDLMETVNNLLTMNSTNSKDPYAKKEQISF 280
Qy 148 LDCPTIKDTIGSVTKTPGVTYIHPEGSSYPREVMCDMDYRGCGTIVYIOKRDIIDFOR 207
Db 261 RDCAVEFVS-----GHTTGITYLTPNSTEELKATCDMEAGGGWTTIQRDDGVDYDOR 336
Qy 208 LWCVDYLDGFDGLGFEWLGKIKFYIYNQKTSFMLVYVALESEDDTLAYASYDNWLEDE 267
Db 337 TWKEKVFYFGNSGEYVWGNFVSLTNQOR--YVLKITHLKMENENAYSLTEHRYLSE 394
Qy 268 TRFFPMHLGRISGNAGDAFRGLKEDNONAMPFSTSDVNDGCRPACLVNGSVKSCSHL 327
Db 395 ELNRYRIHLKGLTGAKI-----SSISOPGNDFTKDGDNKC-----ICKSQM 439
Qy 328 HNKQWMENEGIANLNGIH---FSGRLATLGIONGTWTKNNSPVKIKSYSMKIR 380
Db 440 LT-GGWMFDACGPSWNLNGMYTPQRONTKF--NGIKWYV--KGSIGSLKATYTMIR 491

RESULT 12
Q43827 PRELIMINARY; PRT; 346 AA.
ID Q43827
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AC Q43827;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE CDP6 (ANGIOPOIETIN-LIKE FACTOR) (CDP6 PROTEIN).
GN D3647M16.1 OR CDP6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=CORNEA.
RA Peek R., van Gelderen B.E., Bruijnenberg M., Kijlstra A.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Baguley C.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=SKIN, AND MELANOMA;
RA Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=21318995; Pubmed=11426320;
RA Stover C., Endo Y., Takahashi M., Lynch N., Constantinescu C.,
RA Vorup-Jensen T., Thiel S., Friedl H., Hankeln T., Hall R., Gregory S.,
RA Fujita T., Schwaeble W.;
RT "The human gene for mannan-binding lectin-associated serine protease-2
RT (MASP-2), the effector component of the lectin route of complement
RT activation, is part of a tightly linked gene cluster on chromosome
RT 1p36.2-3.";
RL Genes Immun. 2:119-127(2001).
DR EMBL; Y16132; CAA76078.1; -.
DR EMBL; AL049653; CAB84734.1; -.
DR EMBL; BC001881; AAH01881.1; -.
DR EMBL; AJ300188; CAC15571.1; -.
DR HSSP; P02671.1F2D.
DR InterPro; IPR002181; Fibrinogen_C.
DR Pfam; PF00147; fibrinogen_C; 1.
DR SMART; SM00186; FBG; 1.
SQ SEQUENCE 346 AA; 40018 MW; AEC0A601CC498B43 CRC64;

Query Match 18.1%; Score 380; DB 4; Length 346;
Best Local Similarity 27.9%; Pred. NO. 4.2e-24;
Matches 107; Conservative 67; Mismatches 138; Indels 72; Gaps 15;

Qy 14 VCIFTCGEVQNCVHNSTSSVYNIVEDGSNAKDESKNDTVCKEDCESCDVTKIT- 72
Db 12 LCIFFVAVY-----SHPAWLQKLSKHKTPAQQLKAAN--C---CEEVKEKQAVAN 58
Qy 73 -----REKHFMCNRNLQNSIVSYSTRSKILRRNMDEQOASLDYLSNQVVELMNR 122
Db 59 LSSLSELNKKQGERDWSVYVQ---VMELESNKRMEERLDAESKYSEMNQIDIMQLQ 115
Qy 123 VLLTTEVERKQLDQDPFRRPVQSHGLDCTDIKD---TGSVYTKRPSGLYIHPGSSYPF 179
Db 116 AAQYVQTQTSADAI-----YDCSSLYQKKRYRISGYKRLPPDFLGSF-----L 158
Qy 180 EVMCDMDYRGGWVYIQRIDGIDFQRLMCDYLDGFDGLGFEWLGKIKFYIYNQKNT 239
Db 159 EYFCDMETSGGGWTTIQRKRSGLVSFYDMQYQKGFSGISGDFWLGMEHIIHRLSRQPT- 217
Qy 240 SFMLVYVALESEDDTLAYASYDNFWEDETREFPKMHLGRISGNAG--DARGLKEDNONAM 298
Db 218 --RLRVEWEDWEGNLRVAYEYSHFYVGNELNSYRLFGLGYTGVNDALQ-----YHNNT 269
Qy 299 PESTSDVDNDGCRPACLVNGSVKSCSHLNKQWMENEGIANLNGIHHSFGK--LLAT 356
Db 270 AFSTKDKDNDNC-----LDKCAQL-RKGGYWNCCCTDSNLNGVYIRGEHNKHL 318
```



OY 357 G10MGWTGNKNSPVKIKSVSMKIR 380  
 DB 319 G1TWYGM--H0STYSLKREVKIR 340

## RESULT 13

0902D2  
 ID 09D2D2 PRELIMINARY; PRT; 496 AA.  
 AC 09D2D2  
 DT 01-JUN-2001 (TREMBlrel. 17, Created)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
 DE 11 DAYS PREGNANT ADULT FEMALE OVARY AND UTERUS CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY, CLONE:5031400E18, FULL INSERT SEQUENCE.  
 GN AGPT2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_Taxid=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=OVARY, AND UTERUS;  
 RX MEDLINE=21085660; PubMed=11217851;  
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arikawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H., Kuehl P., Lewis S., Matsuo Y., Nkaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Boffelli D., Bolunga N., Carlini P., de Bonaldo M.F., Blake J., Boffelli D., Bolunga N., Carrin P., de Bonaldo M.F., Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hoffman M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L., Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kontsuki S., Hayaishizaki Y.  
 RT "Functional annotation of a full-length mouse cDNA collection."  
 RL Nature 409:685-690(2001).  
 DR EMBL: AK019860; BAB31887.1;  
 DR HSSP: P02671.1FZD.  
 DR MGD: MGI:102890; Agpt2.  
 DR InterPro: IPR002181; Fibrinogen\_C.  
 DR Pfam: PF00147; fibrinogen\_C.1.  
 DR SMART: SM00186; FBG.1.  
 DR PROSITE: PS00514; FIBRIN\_AG\_C\_DOMAIN.1.  
 SQ SEQUENCE 496 AA; 56575 MW; E7563B498A0EF331 CRC64;

Query Match 18.0%; Score 379.5; DB 11; Length 496;  
 Best Local Similarity 25.7%; Pred. No. 7,4e-24;  
 Matches 111; Conservative 71; Mismatches 125; Indels 125; Gaps 16;

OY 23 V0GCVHSHDSSVNVIVEDGSAKDESKSNDIYCKEDCESCVYKIRITREKNHFCRN 82  
 DB 112 IQQWVQNT---AVVIEIGTSLNQTAA-----QTRKLTVEVQAVQNTLRLEQL 160  
 OY 83 L0NSIVYSTRSTKRLKLNMMDEQASLDYLSNOVNEIMNRVLLTTEVF----- 131  
 DB 161 LQHSI-----STNKLKQIIDD-----TSEINKLQNKSFLEQKVLDMEGKHSQLO 207  
 OY 132 -----RKQ---LDPPHPRV-----OSHGLDCTDIDKDTIGSVTK-- 162  
 DB 208 SMKQKDELQVLVSGKSSVIDELEKLVTAFTVNSLLQKQOH-----DIWETVNSLLTMM 262  
 OY 163 -----TPSGLYIIHPGSSYPREVWCDMPRGCGW 192  
 DB 263 SSPNSKSSVAIRKEQOTTFRDCAIEFKSGLTSTGTYTLTPNPSTEIKAYCDMDVGGGW 322

OY 193 TVIOKRIDGIIDPQRLMCDYLDGFGDILGEEFWLGKIKFYIVNQKNKNSFMLEVLESDD 252  
 DB 323 TVIOHREDGSDVDFORTWKEYKEGFSPLGEYWLGNFVSQLTGHR--YVLIKQDKMEG 380  
 OY 253 TLVAYSVDNFWLEDETRFEKKNHILGRYSGNAGDAERGLAKEDNONAMPSTSDVNDGCRP 312  
 DB 381 NEAHSIVDHFVLAGESNRYRIHLTGIGTACKI-----SSISQPGSDSTSDSDNDC-- 433  
 OY 313 ACLVNGOSVSKCSHLNKTGMFWFNECGLANINGHH-----FSKLLATG10MGWTGNKNS 368  
 DB 434 -----ICKSQSMLS-GWMPDACPNSLNGOYYPQKQNTNRF--NGIKWYW--KGS 480  
 OY 369 PVKIKSVSMKIR 380  
 DB 481 GYSLKATTMTMR 492

## RESULT 14

0908W7  
 ID 0908W7 PRELIMINARY; PRT; 316 AA.  
 AC 0908W7  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
 DE TECHYLECTIN-5B  
 OS Tachyleus tridentatus (Japanese horseshoe crab).  
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;  
 OC Limulidae; Tachyplesus.  
 OX NCBI\_Taxid=6853;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99398666; PubMed=10468566;  
 RA Gokudoe Y., Muta T., Tsuda R., Koori K., Kawahara T., Seki N., Mizunoe Y., Wai S.N., Iwanaga S., Kawabata S.  
 RT "Horseshoe crab acetyl group-recognizing lectins involved in innate immunity are structurally related to fibrinogen."  
 RL Proc. Natl. Acad. Sci. U.S.A. 96:10086-10091(1999).  
 DR EMBL: AB024738; BAB84189.1;  
 DR HSSP: P02671.1FZD.  
 DR InterPro: IPR002181; Fibrinogen\_C.  
 DR Pfam: PF00147; fibrinogen\_C.1.  
 DR SMART: SM00186; FBG.1.  
 DR PROSITE: PS00514; FIBRIN\_AG\_C\_DOMAIN.1.  
 SQ SEQUENCE 316 AA; 36112 MW; 6FFBFEFDA159EDFID CRC64;

Query Match 18.0%; Score 378.5; DB 5; Length 316;  
 Best Local Similarity 29.3%; Pred. No. 5e-24;  
 Matches 113; Conservative 45; Mismatches 117; Indels 111; Gaps 15;

OY 9 LLEFLNVCFTIGEYVQNCVHH---STDSSVNVIVEDGSAKDESKSNDIYCKEDCES 64  
 DB 16 LSFCLVSLVAGD-----YHNHAACSTVCSLKLGLSDVSPLDLAKR----- 58  
 OY 65 CDVTKITRREKHNMCNRLQNSIVSTRSTKLLRNMMDEQASLDYLSNOVNEIMNRV 124  
 DB 59 -----LATLQNPICSKDAF-----YMETYTNQNK-- 85  
 OY 125 LLTTEVERKQLDPPHPRVQSHGL--DCTDIKDTIGSVTKTPSGLYIIHPGSSYPREVW 182  
 DB 86 -----AEKNGLPINCA-----IVYQGNSTSGIYMWPLFLNHPISVF 123  
 OY 183 CDMYRGCGWTVIOKRID--GIIDPQRLMCDYLDGFGDILGEEFWLGKIKFYIVNOKNT 239  
 DB 124 CDMETAGGWTVIQKRGFGOPIONFYOTWESYKNGFENLKEFEKLLIFVLTNO--D 181  
 OY 240 SFMLVYVALESDDTLVAASYDNFWLEDETRFEKKNHILGRYSGNAGDAERGLAKEDNONAMP 299  
 DB 182 SYVLRVLDLEDFEGGRRAEAVEFLVRSLETLYKKSFTYKGDAGDSL-----SOHNMP 235  
 OY 300 FSTSDVDNDGCRPACLVNGOSVSKCSHLNKTGMFWFNECGLANINGI-----HHFSGLK 354

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Db      236  FTTTRDRND-----KMEKNCALAY-KGGWNYNACHHSNLNGMYLRGPHDES---- 280

QY      355  ATGIQMGTVTKNNSPYKIKSYMKIR 380
        | | | | | : | : | | |
Db      281  AVGVNMYQWRGHNSLKYK--EMKIR 304

```

Search completed: May 22, 2002, 15:13:27  
Job time: 359 sec

Q9DER1	RESULT	15
ID Q9DER1	PRELIMINARY;	PRT; 407 AA.
DT 01-MAR-2001 (TREMBLrel. 16, Created)		
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)		
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)		
DE ANGIOPOIETIN-2B.		
GN ANGIOPOIETIN-2B.		
OS Gallus gallus (Chicken).		
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC Actinopterygii; Cyprinodontiformes; Poeyotrichidae; Phasiandae; Phasiandae;		
OC Gallus.		
OX NCBI_TaxID=9031;		
RN [1]		
RP SEQUENCE FROM N.A.		
RX MEDLINE=20422311; PubMed=10964717;		
RA Mezquita J., Mezquita P., Montserrat P., Mezquita B., Francone V.,		
RA Villagrasa X., Mezquita C.;		
RT "Genomic structure and alternative splicing of chicken angiotensin-		
RT 2.";		
RL Biochem. Biophys. Res. Commun. 275:643-651(2000).		
DR EMBL; AJ289778; CAC08175.1; -.		
DR HSSP; P02671; 1F2D.		
DR InterPro; IPR002181; Fibrinogen_C.		
DR Pfam; PF00147; fibrinogen_C; 1.		
DR SMART; SM00186; FBG; 1.		
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.		
Q9 SEQUENCE 407 AA; 46687 MW; 8863BA0AB8C7A41C CRC64;		

Query Match	18.0%	Score 378.5	DB 13	length 407
Best Local Similarity	26.4%	Pred. Nc. 6.9e-24		
Matches 112; Conservative	68;	Mismatches 135;	Indels 109;	Gaps 17;

QY	23	VQNCJAHHSDDSSVNNIVEDGSSNAKDESKSNDYCYCKEDCESODCVKTRIREKHFNCRN	82
Db	23	IQCAVAVONOT----AVNIETGTLINLOT-----AEQTRKLDVYEAQVLAQNTTRELQL	71
QY	83	LQNSIVSYTRSTKLLR-----NMDEQASLDYLSNOVNET-----	119
Db	72	LEHSL-----STNKLREQISVQTEINRILQEKNSFLEKRYLEMDKHTQLKSIKEDQ	126
QY	120	-----MNYVL-----LTTTEFRQOLDPFRPIRYOS--HGL-----	148
Db	127	LQVLVARONSIIEBLEKQLYATATANNSSVLOKQOHDLEIYHNHLTMTI SPNSAKKNE IAK	186
QY	149	-----DCTD-IKDTIGSVYTKPPSGLYIIHPGESSYXPFEVMDMDYRGSGWTVYOKRID	200
Db	187	EQGISFKDCAEAFKSGL-----TTSGIYTLTFPRPSAQEKAYCDOMESGGGWYVLOQRED	241
QY	201	GIDFQRLMCDYLDGFBEDLDGFEPLGLKKTFFIYVNOKNTSMFLVLALESDDTLATASTD	260
Db	242	GSDVDFHTWKEYKIGFEDDPAGEVYLGNEFPYSOLTNOKR--YVLKILIKLDEGNEAYTLVD	299
QY	261	NFWLEDETRFPEKMHLYGYSNAGACAFGLKEDQONAMPRTSPSDVNDGCRPACLVNGOS	320
Db	300	QFYLANEQKRYRIHLKQLTGTACKI-----SSISQPGNDSTKADADMDKC-----	344
QY	321	VKSCSLHNKTMGMFNCEGLANLNGIH-----FSGKLATGIQMGTTKNSPVIKTSVS	376
Db	345	ICKOSQMLT--GGMWFDACGPSNLNGWYPLRQNNKKF--NGIKWYV--RGSGVSLKATTT	399
QY	377	MKIR	380
Db	400	MMIR	403

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: May 22, 2002, 15:07:58 ; Search time 17.4 Seconds  
(without alignments)  
863.401 Million cell updates/sec

Title: US-09-596-196-4

Perfect score: 2104

Sequence: 1 MMSPSQSLFLFANVCIFTCG.....PVKIKSVSMKIRMYNPFYK 388

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	413.5	19.7	439	1 FGL2_HUMAN	Q14314 homo sapien
2	405.5	19.3	432	1 FGL2_MOUSE	P12804 mus musculu
3	400.5	19.0	481	1 AGR1_BOVIN	O18920 bos taurus
4	400.5	19.0	493	1 ANL2_MOUSE	O9r045 mus musculu
5	400	19.0	493	1 ANL2_HUMAN	O9uk99 homo sapien
6	398	18.9	312	1 FGL1_HUMAN	O08830 homo sapien
7	395.5	18.8	468	1 FIBB_BOVIN	P02676 bos taurus
8	395	18.8	498	1 AGR1_HUMAN	O15389 homo sapien
9	391	18.6	498	1 AGR1_MOUSE	O08538 mus musculu
10	381.5	18.1	496	1 AGR2_HUMAN	O15123 homo sapien
11	375.5	17.8	491	1 FIBB_HUMAN	P02675 homo sapien
12	375	17.8	375	1 AGR2_BOVIN	O77802 bos taurus
13	374.5	17.8	496	1 AGR2_MOUSE	O35608 mus musculu
14	373.5	17.8	479	1 FIBB_RAT	P14480 rattus norv
15	371.5	17.7	463	1 FIBB_CHICK	O02020 gallus gall
16	370	17.6	477	1 FIBB_PETMA	P02678 petromyzon
17	367.5	17.5	443	1 FIBG_HUMAN	P02679 homo sapien
18	365	17.3	454	1 FIBG_BOVIN	P12799 bos taurus
19	363	17.3	432	1 FIBG_PETMA	P04115 petromyzon
20	360	17.1	509	1 AGR4_MOUSE	O9wv76 mus musculu
21	358	17.0	503	1 AGR4_HUMAN	O9y674 homo sapien
22	353	16.8	438	1 FIBG_XENLA	P17634 xenopus lae
23	351	16.7	319	1 FCN2_RAT	P57756 rattus norv
24	350.5	16.7	282	1 FIBB_PARPA	P19477 parastichop
25	348.5	16.6	774	1 FIBB_DROME	P21620 drosophila
26	337.5	16.0	866	1 FIBB_HUMAN	P02671 homo sapien
27	335.5	15.9	741	1 FCN2_CHICK	P14448 gallus gall
28	332	15.8	306	1 FCN2_MOUSE	O70497 mus musculu
29	329.5	15.7	641	1 FCN2_PETMA	P33573 petromyzon
30	329	15.6	334	1 FCN1_MOUSE	O70165 mus musculu
31	327.5	15.6	445	1 FIBG_RAT	P02880 rattus norv
32	321.5	15.3	313	1 FCN2_HUMAN	O15485 homo sapien
33	321	15.3	255	1 MFA4_HUMAN	P55083 homo sapien

34	313.5	14.9	782	1 FIBB_RAT	P06399 rattus norv
35	310.5	14.8	1808	1 FCN1_CHICK	P10039 gallus gall
36	305.5	14.5	335	1 FCN1_RAT	O9wv88 rattus norv
37	303.5	14.4	326	1 FCN1_HUMAN	O00602 homo sapien
38	302.5	14.4	4289	1 FCN3_HUMAN	P22105 homo sapien
39	291	13.8	299	1 FCN3_HUMAN	O75636 homo sapien
40	282.5	13.4	1746	1 FCN2_PIG	O29116 sus scrofa
41	271	12.9	2201	1 FCN2_HUMAN	P24821 homo sapien
42	197	9.4	137	1 AGR2_RAT	O35462 rattus norv
43	109	5.2	129	1 MFA4_BOVIN	P55918 bos taurus
44	99.5	4.7	586	1 PMEL_ARATH	O43867 arabidopsis
45	99	4.7	599	1 YAOB_SCHPO	O10110 schizosacch

## ALIGNMENTS

```

RESULT 1
FGL2_HUMAN          STANDARD:      PRT:   439 AA.
ID      FGL2_HUMAN
AC      Q14314;
DT      16-OCT-2001 (Rel. 40, Created)
DT      16-OCT-2001 (Rel. 40, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Fibrinoleukin precursor (Fibrinogen-like protein 2) (PT49).
GN      FGL2
OS      Homo sapiens (human).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX      NCBI_Taxid=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Small intestine;
RX      MEDLINE=95369700; PubMed=7642106;
RA      Ruegg C., Pytela R.;
RT      "Sequence of a human transcript expressed in T-lymphocytes and
RL      encoding a fibrinogen-like protein.";
RN      Gene 160:257-262(1995).
RN      [2]
RP      SEQUENCE FROM N.A.
RA      Yvwarej S., Liu M., Marsden P., Levy G.;
RT      "Cloning and characterization of Hfg12: the human counterpart to the
RL      mouse gene Fgl2.";
RN      Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
RN      [3]
RP      CHARACTERIZATION.
RX      MEDLINE=98309432; PubMed=9647217;
RA      Marazzi S., Blum S., Hartmann R., Gundersen D., Schreyer M.,
RA      Argraves S., von Fliedner V., Pytela R., Ruegg C.;
RT      "Characterization of human fibrinoleukin, a fibrinogen-like protein
RT      secreted by T lymphocytes.";
RN      J. Immunol. 161:136-147(1998).
RN      [4]
RP      FUNCTION: MAY PLAY A ROLE IN PHYSIOLOGIC LYMPHOCYTE FUNCTIONS AT
CC      MUCOSAL SITES.
CC      - SUBUNIT: HOMOTETRAMER; DISULFIDE-LINKED.
CC      - SUBCELLULAR LOCATION: Secreted.
CC      - TISSUE SPECIFICITY: CONSTITUTIVELY EXPRESSED IN CYTOTOXIC
CC      T-CELLS.
CC      - SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      EMBL: Z36531; CAAB5298.1;
CC      EMBL: AF104015; AADI0825.1;
CC      EMBL: AF104014; AADI0825.1; JOINED.
CC      HSSP: P02671; 1FZD.
CC      MIM: 605351;
DR

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DR InterPro: IPR002181: fibrinogen_C.
DR Pfam: PF00147; fibrinogen_C; 1.
DR SMART: SM00186; FBG; 1.
DR PROSITE: PS00514; FIBRIN_AG_C_DOMAIN; 1.
KW T-cell; Glycoprotein; Signal.
FT SIGNAL 1 23
FT CHAIN 24 439
FT DOMAIN 210 435
FT DISULFID 213 442
FT DISULFID 371 384
FT CARBOHYD 25 25
FT CARBOHYD 179 179
FT CARBOHYD 235 235
FT CARBOHYD 263 263
FT CARBOHYD 336 336
SQ SEQUENCE 439 AA; 50228 MW; DF34656288E49E68 CRC64;

Query Match 19.7%; Score 413.5; DB 1; Length 439;
Best Local Similarity 30.28; Pred. No. 1.5e-25;
Matches 119; Conservative 61; Mismatches 147; Indels 67; Gaps 15;

QY 34 SSVYVIVEDSGSNMAKDESKNDYVCKEDCE-----ESCQVTK 70
DB 73 SRLEVEFKEVQNKLEIVNSLKKSC-QQCKIQADNDGPRNGLLPSTGARGEVGDNRVR 131
QY 71 ITREKRFMCRLNLS-----IVSTRSTKTLRLRM-----MDEQASLDYLSQVNELM 120
DB 132 ELSEVFNKLSSELNKAEIVNLHGRREKLLVNMNNIENYVDSKVALNLTFFVNSLDKSC 191
QY 121 NRVLTLTEVFRKQLDFFRHPVOSHGL--DCTDIKDTIGSVTKTPPSGLYIIHEGSSYP 178
DB 192 SKC-----PSQEQIQSRPVQ-HILYKDCSDY---AIGKRSSSTYVTPDPKNSS 237
QY 179 FEVACMDYRGKGVTVQIKRIDIFQRLWCYLDLGGDLGSEFWLGLKIFYIVNQKN 238
DB 238 FEVYCDMETGSGGWTQVQARLDGSTNFTRMQDYKAGGNNRREPLGNDGIHLIT--KS 295
QY 239 TSPMLIYALSEDDTLAYASDINFWLEDETRFFKMLIGRYSGNAGDAFRGLKKEDNONAM 298
DB 296 KEMILRIDLEDNFQVLELYALYDQFYVANEFLKRLHGVNNGTAGDALR-FNKHVNHDLK 354
QY 299 PFSTSDVNDGCRPACLVNGQSVKCSHLNKTGMWFEGLANLNG-IHFSCKLATGTG 357
DB 355 FETTPDKDNDRIYPSG-----NCG-LYSSGMWFDACLSAINDKYYTHQKTRGVANG 404
QY 358 IOMGTW--TRNNSEPKIKRYSMKIRMYNP-YFK 388
DB 405 IFMGITWGVSEAHHPGYSKSFKEAKMMIRPKHF 438

RESULT 2
FGL2_MOUSE STANDARD; PRT; 432 AA.
AC P12804;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cytotoxicin precursor (fibrinogen-like protein 2) (Prothrombinase)
DE (Cytotoxic T-lymphocyte specific protein).
GN FGL2 OR FIBLP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Cytotoxic T-cell;
RA MEDLINE=87175327; PubMed=3550794;
RA Royama T., Hall L.R., Haase W.G., Tonegawa S., Saito H.;
RT "Structure of a cytotoxic T-lymphocyte-specific gene shows a strong
RT homology to fibrinogen beta and gamma chains.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:1609-1613(1987).
```

```
RM [2]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC STRAIN-BALB/CJ; TISSUE-peritoneal macrophage;
RX MEDLINE=95333285; PubMed=7609073;
RA Parr R.L., Fung L., Reneker J., Myers-Mason N., Leibowitz J.L.,
RA Levy G.;
RT "Association of mouse fibrinogen-like protein with murine hepatitis
RT virus-induced prothrombinase activity.";
RL J. Virol. 69:5033-5038(1995).
CC -1 FUNCTION: CONVERTS PROTHROMBIN TO THROMBIN.
CC -1 SUBUNIT: HOMOTETRAMER; DISULFIDE-LINKED (BY SIMILARITY).
CC -1 SUBCELLULAR LOCATION: Secreted.
CC -1 TISSUE SPECIFICITY: CONSTITUTIVELY EXPRESSED IN CYTOTOXIC
CC T-CELLS.
CC -1 INDUCTION: IN MACROPHAGES, DURING INFECTION BY MOUSE HEPATITIS
CC VIRUS STRAIN 3 (MHV-3).
CC -1 SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: M16238; AAA37624.1; -.
DR EMBL: M15761; AAA37624.1; JOINED.
DR EMBL: S78773; AAA34823.1; -.
DR PIR: A27447; A27447.
DR HSSP: P02671; 1FZD.
DR MCD: MGI103266; Fgl2.
DR InterPro: IPR002181; Fibrinogen_C.
DR Pfam: PF00147; fibrinogen_C; 1.
DR SMART: SM00186; FBG; 1.
DR PROSITE: PS00514; FIBRIN_AG_C_DOMAIN; 1.
KW T-cell; Cytolysis; Signal.
FT SIGNAL 1 19
FT CHAIN 20 432
FT DOMAIN 203 428
FT DISULFID 206 235
FT DISULFID 364 377
FT CARBOHYD 24 24
FT CARBOHYD 172 172
FT CARBOHYD 228 228
FT CARBOHYD 256 256
FT CARBOHYD 329 329
FT CONFLICT 332 332
SQ SEQUENCE 432 AA; 48951 MW; 2B297F69CBA4782 CRC64;

Query Match 19.3%; Score 405.5; DB 1; Length 432;
Best Local Similarity 35.4%; Pred. No. 6.2e-25;
Matches 110; Conservative 43; Mismatches 115; Indels 43; Gaps 13;

QY 98 LRNMDEQQA-----SLDYLSQVNELMNRVLLTTEVFRKQD-----PFP 139
DB 137 LKNMADQIQLOGRLLETLVLMNNIENYVDNKNVLTVVV--NSLDCKSCSPQSEHQ 194
QY 140 HRPVOSHGL--DCTDIKDTIGSVTKPSGLYIIHEGSSYPEVWCMDYRGKGVTVQK 197
DB 195 SOPVQ-HILYKDCSD-HYVLG---RRSSGAYRVTPDHRNSSFETVCDMETMGGWTVLQA 249
QY 198 RIDGIIDFQRLWCYLDLGGDLGSEFWLGLKIFYIVNQKTSFMYALASEDDTLAYV 257
DB 250 RLDSSTNFTREKQKQKAFGNERNERFWLGNKIHLLT--KSEMLIRLRLDLEFNGTLTYA 307
QY 258 SYDNFWLEDETRFFKMLIGRYSGNAGDAFRGLKKEDNONAMPSTSDVNDGCRPACLVN 317
DB 308 LYDQGVYANVELFLKRYLHIGVNGTAGDALR-FSRHYNHDLREFTPDRDNDRIYPSG---- 362
QY 318 GQSVKSCSHLKNKTGMWNEGLANLNG-IHFSCKLATIGIQMTWTKNN--SVVKIKS 374
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FT	CARBOHYD	294	294	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	NON_TER	481	481	
SO	SEQUENCE	481 AA;	53556 MW;	BEECEDB4FC2BB50 CRC64;
	Query Match	19.0%	Score 400.5;	DB 1; Length 481;
	Best Local Similarity	27.9%	Pred. No. 1.8e-24;	
	Matches 114;	Conservative 60;	Mismatches 116;	Indels 119; Gaps 15;
QY	23 VQNCVHSHSTDSVYNIYEDGSNAKDESKSDNYCCKEDCEESCDVKTKITREKHFMCRN 82			
DB	115 IQQNAVQVHHT-----ATMLEIGTSLLSQ-----AEQTRKLTVEYQVNLQTSRLQQL 163			
QY	83 LQNSIVSY-----			
DB	164 LENSISTYKLEKQLDQQTNEILKIHENKSLLEHKIFEMEGKHKEEDLTDLKEEKENLQGLV 223			
QY	103 DEQASLDYLSNVN-----ELM-----NVLLLTTEVF-----RKQDPEP 139			
DB	224 TRQYVYIOELEKQLRATITNNSVLOKQOOLEMDYVHNLVNLCTQTEVLKLGSKRRKEEPF- 282			
QY	140 HRPVQSHLDCTDITDITIGSYTKTPSGGLYIHPBESSYPFVCMCDMGGRGWYIQKRI 199			
DB	283 -----RDCADY-----QACFKNSGITYITTYINMPKPKVPCFCDMDLNGSGWYIQHRE 330			
QY	200 DGIIDFQRLMCDYLDGFGDLLGEFLLGLKIFLYIVNKNSTFEMLYVALESDPTLVAASY 259			
DB	331 DGSILDFQGWKEKYKMGFNPSPGEWYLGNEFIPTLSQR--QYTLRIELLDWEGNRAVYQY 388			
QY	260 DNFMLEDETRFFKMHGLGKSGNAGDAFGLKKEED--ONAMPFSTSDVNDGCRPAC--L 315			
DB	389 DRFHNGEKQVNRRLYKLTGHTGTAG-----KQSLILHGAADFSTKDDNDNCMKCKAL 441			
QY	316 VNGQSVKSCSHLNKTKGMPNECCGANTNGIHNS-----GKLTATGIOW 360			
DB	442 LFG-----GMPFDACGSPNLMGMPYTAGQNHKRL--NGIKW 475			
RESULT 4				
ANL2_MOUSE				
ID	ANL2_MOUSE	STANDARD:	PRT:	493 AA.
AC	O9R045:			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	01-MAR-2002 (Rel. 41, Last annotation update)			
DE	Angiopoietin-related protein 2 precursor (Angiopoietin-like 2).			
GN	ANGPTL2 OR ARP2.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.			
OX	NCBI_Taxid=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Heart.			
RX	MEDLINE=99403103; PubMed=10473614;			
RA	Kim I., Moon S.-O., Koh K.N., Kim H., Uhm C.-S., Kwak H.J., Kim N.-G.,			
RA	Koh G.-Y.;			
RT	"Molecular cloning, expression, and characterization of angiopoietin-			
RT	related protein. angiopoietin-related protein induces endothelial cell			
RT	sprouting.";			
RL	J. Biol. Chem. 274:26523-26528(1999).			
CC	-1- FUNCTION: INDUCES SPROUTING IN ENDOTHELIAL CELLS THROUGH AN			
CC	AUTOCRINE AND PARACRINE ACTION (BY SIMILARITY).			
CC	-1- SUBCELLULAR LOCATION: Secreted (By similarity).			
CC	-1- TISSUE SPECIFICITY: WIDELY EXPRESSED IN HEART, TONGUE, LUNG AND			
CC	SKELETAL MUSCLE. ALSO FOUND IN LOWER LEVELS IN KIDNEY, EPIDIDYMOUS			
CC	AND TESTIS.			
CC	-1- SIMILARITY: CONTAINS 1 FIRINOGEN C-TERMINAL DOMAIN.			
CC	-----			
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DE related protein 1) (HFRP-1) (Hepassocin) (HP-041).  
GN FGL1 OR HFRP1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
CC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
OX NCBI\_TaxID=9606.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE-Liver:  
RX MEDLINE=93290661; PubMed=8390249;  
RA Yamamoto T., Gotoh M., Sasaki H., Terada M., Kitajima M.,  
RT Hirohashi S.;  
RT "Molecular cloning and initial characterization of a novel  
RT fibrohem-related gene, HFRP-1.";  
RL Biochem. Biophys. Res. Commun. 193:681-687(1993).  
RN [2]  
RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.  
RC TISSUE-Liver:  
RX MEDLINE=21363035; PubMed=11470158;  
RA Hara H., Yoshimura H., Uchida S., Toyoda Y., Aoki M., Sakai Y.,  
RT Morimoto S., Shiohama K.;  
RT "Molecular cloning and functional expression analysis of a cDNA for  
RT human hepassocin, a liver-specific protein with hepatocyte mitogenic  
RT activity.";  
RL Biochim. Biophys. Acta 1520:45-53(2001).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE-Liver:  
RA Strausberg R.;  
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: Has hepatocyte mitogenic activity.  
CC -!- SUBUNIT: Homodimer (probable).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Liver-specific.  
CC -!- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.  
-----  
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CC  
DR EMBL: D14446; BAA03336.1; -;  
DR EMBL: D87342; BAB70690.1; -;  
DR EMBL: BC007047; AAH07047.1; -;  
DR MIM: 605776; -;  
DR HSSP: P02671; 1FZD.  
DR InterPro: IPR002181; Fibrinogen\_C.  
DR Pfam: PF00147; Fibrinogen\_C; 1.  
DR SMART: SM00186; FBG; 1.  
DR PROSITE: PS00514; FIBRIN\_AG\_C-DOMAIN; 1.  
KW Signal.  
FT SIGNAL. 1 22  
FT CHAIN 23 312 FIBRINOGEN-LIKE PROTEIN 1.  
FT DOMAIN 78 305 FIBRINOGEN C-TERMINAL.  
FT DISULFID 26 26 INTERCHAIN (POTENTIAL).  
FT DISULFID 83 112 BY SIMILARITY.  
FT DISULFID 248 261 BY SIMILARITY.  
FT CONFLICT 15 15 I -> T (IN REF. 3).  
FT CONFLICT 69 69 N -> D (IN REF. 1).  
FT CONFLICT 72 72 I -> V (IN REF. 1).  
FT CONFLICT 105 105 P -> L (IN REF. 2).  
FT CONFLICT 312 AA; 36391 MW; 26BC82124E6660C2 CRC64;  
SQ SEQUENCE

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Query Match      18.9% Score 398; DB 1; Length 312;
Best Local Similarity 34.3%; Pred. NO. 1.6e-24;
Matches 111; Conservative 44; Mismatches 115; Indels 54; Gaps 12;
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Db	4	VFSTILTALLI---	KGREISALEDCAQEOEMRLRAOVRLLLETRVKKOQYKILLQENVE	60
Qy	135	--LDPFPHRPVQSHG-----	LDCTDIKDITGVTYKTPSGLIYIHPREGSSYPFEVCMNDY	187
Db	61	QFLDKGDENTYIDIGSKRQYADCS	EIFNDYKL-----SGPYKAKRLQSAEESVYCDMS-	115
Qy	188	RGGGMYVIOKRIIDGIIDPRLMCDY	LDYFGDDL--GFEWLGIKKITYLVNOKNTSFMYL	244
Db	116	DGGGMYVIOKRSDDSENFNMGMKD	YENGFEFNFOAKHGEWLGKLNHFLTQED--YTLK	173
Qy	245	VALSEDDTLAASYDPMFLIEDR	FRFKMLIGYSCNAGDAPFGLKKEDN-----NMMP	299
Db	174	IDLDLDFEKNRSRYADYKKNFKG	DEKNEFYLELNGEISCTAGDSLAGNFHPVQWASHQRK	233
Qy	300	FSTDVDNDGCRPAICLVNGQSVK	SCSHLHKTKTGMWNEEGLANLNGHFSCKLLA--T	356
Db	234	FSTMDRHDNDNEGCAEDDS-----	GMWNRCHSANLNGV--YSSPYTKAKDN	281
Qy	357	GIOMGTWTKNNSPVKIKSVSKMR	380	
Db	282	GIWVYTW--HGMWYLSKVYMKIR	303	
RESULT	7			
FIBB_BOVIN		STANDARD;	PRT;	468 AA.
ID				
AC	P02676;			
DT	21-JUL-1986 (Rel. 01,	Created)		
DT	01-FEB-1996 (Rel. 33,	Last sequence update)		
DT	01-MAR-2002 (Rel. 41,	Last annotation update)		
DE	Fibrinogen beta chain precursor	[Contains: fibrinopeptide B].		
GN	FCB.			
OS	Os taurus (Bovine).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;			
OC	Bovidae; Bovinae; Bos.			
OX	NCBI_TaxID=9913;			
RN	[1]			
RP	SEQUENCE OF 1-4.			
RA	Blomback B., Doolittle R.F.;			
RT	"The sequence of amino acids at the N-terminal end of bovine			
RL	fibrinopeptide B."			
RL	Acta Chem. Scand. 17:1816-1819.(1963).			
RN	[2]			
RP	SEQUENCE OF 5-21.			
RA	Stoquist J., Blomback B., Wallen P.;			
RT	"Amino acid sequence of bovine fibrinopeptides."			
RL	Ark. Kemi 16:425-436.(1960).			
RN	[3]			
RP	SEQUENCE OF 22-53.			
RX	MEDLINE=79164394; PubMed=434821;			
RA	Matthielli R.A., Inglis A.S., Rubira M.R., Hageman T.C.,			
RA	Hurrell J.G.R., Leach S.J., Scheraga H.A.;			
RT	"Amino acid sequences of portions of the alpha and beta chains of			
RL	bovine fibrinogen."			
RL	Arch. Biochem. Biophys. 192:27-32.(1979).			
RN	[4]			
RP	SEQUENCE OF 44-468 FROM N.A.			
RX	MEDLINE=81199473; PubMed=6262803;			
RA	Chung D.W., Rixson M.W., McGillivray R.T.A., Davie E.W.;			
RT	"Characterization of a cDNA clone coding for the beta chain of bovine			
RL	fibrinogen."			
RL	Proc. Natl. Acad. Sci. U.S.A. 78:1466-1470.(1981).			
CC	-1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT			
CC	POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET			
CC	AGGREGATION.			
CC	-1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS			
CC	(ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.			
CC	-1- THROMBIN: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY			
CC	THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA			
CC	CHAINS, AND THIS EXPOSES THE N-TERMINAL POLYMERIZATION SITES			
CC	RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT. THE SOFT CLOT IS			
CC	CONVERTED INTO THE HARD CLOT BY FACTOR XIII WHICH CATALYZES THE			

CC EPSILON-(GAMMA-GLUTAMYL)LYSINE CROSS-LINKING BETWEEN GAMMA CHAINS  
CC (STRONGER) AND BETWEEN ALPHA CHAINS (WEAKER) OF DIFFERENT  
CC MONOMERS.  
CC -----  
CC -1- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL: V00110; CAA23444.1; -.  
CC PIR: A03122; FGBOB.  
CC HSSP: P02675; 1FZA.  
CC InterPro: IPR002181; Fibrinogen\_C.  
CC Pfam: PF00147; fibrinogen\_C. 1.  
CC SMART: SM00186; FBG: 1.  
CC PROSITE: PS00514; FIBRIN\_AG\_C\_DOMAIN; 1.  
CC Blood coagulation; Plasma; Platelet; Glycoprotein; Sulfation.  
CC PEPTIDE 1 21 FIBRINOPEPTIDE B.  
CC CHAIN 22 468 FIBRINOGEN BETA CHAIN.  
CC MOD.RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
CC MOD.RES 6 6 SULFATION.  
CC SITE 21 22 CLEAVAGE (BY THROMBIN; RELEASE  
CC FIBRINOPEPTIDE B).  
CC FT DISULFID 72 72 INTERCHAIN (WITH ALPHA).  
CC FT DISULFID 83 83 INTERCHAIN (WITH ALPHA).  
CC FT DISULFID 87 87 INTERCHAIN (WITH GAMMA).  
CC FT DISULFID 200 200 INTERCHAIN (WITH GAMMA).  
CC FT DISULFID 204 204 INTERCHAIN (WITH ALPHA).  
CC FT DISULFID 208 293 BY SIMILARITY.  
CC FT DISULFID 218 247 BY SIMILARITY.  
CC FT DISULFID 401 414 BY SIMILARITY.  
CC FT CARBOHYD 371 371 N-LINKED (GLCNAC. . .) (PROBABLE).  
CC FT SEQUENCE 468 AA; 53340 MW; 2DED42F443AA4B37 CRC64;  
  
Query Match 18.8%; Score 395.5; DB 1; Length 468;  
Best Local Similarity 27.5%; Pred. No. 4.3e-24;  
Matches 120; Conservative 54; Mismatches 145; Indels 117; Gaps 16;  
  
QY 27 CVHSHDSSVNVIVEDSNKDESKSNDYCKEDCESDVCKITREKHF--MCRNLQ 84  
DB 72 CLHADPLGLV-----CPGCKLDPLVQERIRKSIDLR 108  
QY 85 NSIYSYSTRYK-----LRRNMDEQASLDYLSNOVNELMN-----121  
DB 109 NYVDSVSRSSSTFOYITLLKNNMKGRNOVDNENYVNSSHLEKHQLYIDETVKNKI 168  
QY 122 ----RVLLTTEVERKQLDPP-----HRVQSHGLDCTDIKDTIGS 159  
DB 169 PTKLRVLRSLILENRSKIQKLESQVSTQMEYCRPTCTVTCNIPYVS--GKECEKIIIRNGE 227  
QY 160 VTRPSGLIIHHPGSSYPREVMDMYRGSGWVIOKRIDGIIDFORLMDYDGRDL 219  
DB 228 T-----SEMYLLQRPDSSKPYRVYCDMKTERGKGVWVIONROGSGWPKWDPYQGFQNI 283  
QY 220 L-----GEFMGLKTKIPYIVNOKNTSFMALYALESEDDTLAAYSDNFWLEDE 267  
DB 284 ATNAEGKKYCGVPEYVGLNDRIQLNMGPTK--LLIEMDMKGDVYTALEYEFTYQNE 341  
QY 268 TRFFKMLHGRYSNAGDAF-----RGLKEDN-----QNAPESTSDVDNDCRPACLVNGQ 319  
DB 342 ANKYQLSVSKYKGTAGNALLEGASQLVGENRTWTHINSMFESTYDRDNDGKKT-----D 396  
QY 320 SVKSCSHLHKTKGMWMECCGANLNGIHHSGL-----LATGLOMGWTVKANSFPVK 371  
DB 397 PRKQCSK-EDGGGMMWYRCHAANPNGRYWGAYTWMADKHTDGGVMMNM--QGSWYS 453  
QY 372 IKVSMKIRRMVNPYF 387  
DB 372 IKVSMKIRRMVNPYF 387

DB 454 MKKSMKIR----PYF 465  
  
RESULT 8  
ACPL\_HUMAN STANDARD; PRT; 498 AA.  
ID ACPL\_HUMAN 015389;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 01-MAR-2002 (Rel. 41, Last annotation update)  
DE Angiotensin-1 precursor (ANG-1).  
GN ANGP1 OR KIAA0003.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_Taxid:9606;  
RN [1]  
RP SEQUENCE FROM N.A., AND VARIANT GLY-269 DEL.  
RC TISSUE=Fetal Lung;  
RX MEDLINE=97134663; PubMed=8980223;  
RA Davis S., Aldrich T.H., Jones P.F., Acheson A., Compton D.L., Jain V.,  
RA Ryan T.E., Bruno J., Radzilewski C., Maisonspierre P.C.,  
RA Yancopoulos G.D.;  
RT "Isolation of angiotensin-1, a ligand for the TIE2 receptor, by  
RT secretion-trap expression cloning.";  
RL Cell 87:1161-1169(1996).  
RN [2]  
RP SEQUENCE FROM N.A., Kikuno R., Nomura N.;  
RA Ohara O., Nagase T., submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE OF 307-498 FROM N.A.  
RC TISSUE=Bone marrow;  
RX MEDLINE=96051387; PubMed=7584026;  
RA Nomura N., Miyajima N., Sazuka T., Tanaka A., Kawarabayashi Y.,  
RA Sato S., Nagase T., Seki N., Ishikawa K.-I., Tabata S.;  
RT "Prediction of the coding sequences of unidentified human genes. I.  
RT The coding sequences of 40 new genes (KIAA0001-KIAA0040) deduced by  
RT analysis of randomly sampled cDNA clones from human immature myeloid  
RT cell line KG-1.";  
RL DNA Res. 1:27-35(1994).  
RN [4]  
RP FUNCTION: BINDS AND ACTIVATES TIE2 RECEPTOR BY INDUCING ITS  
CC TYROSINE PHOSPHORYLATION. IMPLICATED IN ENDOTHELIAL DEVELOPMENTAL  
CC PROCESSES LATER AND DISTINCT FROM THAT OF VEGF. APPEARS TO PLAY A  
CC CRUCIAL ROLE IN MEDIATING RECIPROCAL INTERACTIONS BETWEEN THE  
CC ENDOTHELIUM AND SURROUNDING MATRIX AND MESENCHYME. MEDIATES BLOOD  
CC VESSEL MATURATION/STABILITY. IT MAY PLAY AN IMPORTANT ROLE IN THE  
CC HEART EARLY DEVELOPMENT.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- MISCELLANEOUS: IT MAY HAVE A POTENTIAL THERAPEUTIC UTILITY SINCE  
CC IT CAN BE USED FOR SPECIFICALLY TARGETING TUMOR VASCULATURE OR FOR  
CC PROMOTING ANGIOGENIC PROCESSES IN CERTAIN ORGANS SUCH AS AN  
CC ISCHEMIC HEART.  
CC -1- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.  
CC -----  
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CC -----  
CC EMBL: U83508; AAB50557.1; -.  
CC EMBL: D13628; BAA02793.2; ALT\_INIT.  
CC HSSP: P02671; 1FZD.  
CC MIM: 601677; -.  
CC InterPro: IPR002181; Fibrinogen\_C.  
CC Pfam: PF00147; fibrinogen\_C. 1.  
CC SMART: SM00186; FBG: 1.  
CC PROSITE: PS00514; FIBRIN\_AG\_C\_DOMAIN; 1.  
CC Glycoprotein; Coiled coil; Signal; Polymorphism.



Query Match	18.8%	Score 395	DB 1	Length 498
Best Local Similarity	27.0%	Pred. No. 5.1e-24		
Matches 116; Conservative		66; Mismatches 126;	Indels 122;	Gaps 16

RESULT	9		
ACGI_MOUSE	ID	ACGI_MOUSE	STANDARD; PRT; 498 AA.
AC	006538:		
DT	16-OCT-2001 (Rel. 40, Created)		
DT	16-OCT-2001 (Rel. 40, last sequence update)		
DT	16-OCT-2001 (Rel. 40, last annotation update)		
DE	Angiopietin-1 precursor (ANG-1).		
GN	ANGPT1 OR ACPT.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10099;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=97134663; PubMed=8980223;		
RA	Davis S., Aldrich T.H., Jones P.F., Acheson A., Compton D.L., Jain V.,		
RA	Ryan T.E., Bruno J., Radziejewski C., Maisonneville P.C.,		
RA	Vancopoulos G.D.,		
RT	*Isolation of angiopoietin-1, a ligand for the TIE2 receptor, by		

```

RT secretion-trap expression cloning."
RL Cell 87:1161-1168(1996).
CC -I- FUNCTION: BINDS AND ACTIVATES TIE2 RECEPTOR BY INDUCING ITS
CC TYROSINE PHOSPHORYLATION. IMPLICATED IN ENDOTHELIAL DEVELOPMENTAL
CC PROCESSES LATER AND DISTINCT FROM THAT OF VEGF. APPEARS TO PLAY A
CC CRUCIAL ROLE IN MEDIATING RECIPROCAL INTERACTIONS BETWEEN THE
CC ENDOTHELIAL AND SURROUNDING MATRIX AND MESENCHYME. MEDIATES BLOOD
CC VESSEL MATURATION/STABILITY. IT MAY PLAY AN IMPORTANT ROLE IN THE
CC HEART EARLY DEVELOPMENT.
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- DEVELOPMENTAL STAGE: EARLY IN DEVELOPMENT, AT E9 TO E11. IT IS
CC FOUND MOST PROMINENTLY IN THE HEART MYOCARDIUM SURROUNDING THE
CC ENDOCARDIUM. LATER, IT BECOMES MORE WIDELY DISTRIBUTED, MOST OFTEN
CC IN THE MESENCHYME SURROUNDING DEVELOPING VESSELS, IN CLOSE
CC ASSOCIATION WITH ENDOTHELIAL CELLS.
CC -I- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.
CC -----
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CC entities requires a license agreement (see http://www.isb-sib.ch/announce/or-send-an-email-to-license@sib-sib.ch).
CC -----
CC EMBL; U83509; AAB50558.1; -.
CC DR HSSP; P02671; IPFD.
CC DR MGD; MG1:108448; Agpt.
CC DR InterPro; IPR002181; Fibrinogen_C.
CC DR Pfam; PF00147; Fibrinogen_C.1.
CC DR SMART; SM00186; FBG; 1.
CC DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
CC KW Glycoprotein; Coiled coil; Signal.
CC FT SIGNAL 1 19 POTENTIAL.
CC FT CHAIN 20 498 ANGIOPOIETIN-1.
CC FT DOMAIN 81 119 COILED COIL (POTENTIAL).
CC FT DOMAIN 153 261 COILED COIL (POTENTIAL).
CC FT DOMAIN 284 498 FIBRINOGEN C-TERMINAL.
CC FT CARBOHYD 92 92 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 122 122 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 154 154 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 243 243 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SQ SEQUENCE 498 AA; 57505 MW; 285B4FDEC260D800 CRC64;

```



RP SEQUENCE FROM N.A.  
 RA Chung D.W., Harris J.E., Davie E.W.;  
 RT "Nucleotide sequences of the three genes coding for human  
 RT fibrinogen.";  
 RL (in) Liu C.Y., Chien S. (eds.);  
 RL Fibrinogen, thrombosis, coagulation and fibrinolysis, pp.39-48,  
 RL Plenum Press, New York (1991).  
 RN [4]  
 RP SEQUENCE OF 31-491, AND CARBOHYDRATE-LINKAGE SITE.  
 RA Henschen A., Lottspeich F., Southan C., Topfer-Petersen E.;  
 RT "Human fibrinogen: sequence, sulfur bridges, glycosylation and some  
 RT structural variants.";  
 RL (in) Peeters H. (eds.);  
 RL Protides of the biological fluids, Proc. 28th colloquium, pp.51-56,  
 RL Pergamon Press, Oxford (1980).  
 RN [5]  
 RP SEQUENCE OF 31-491.  
 RX MEDLINE=79124640; PubMed=420779;  
 RA Walt K.W.K., Takagi T., Doolittle R.F.;  
 RT "Amino acid sequence of the beta chain of human fibrinogen.";  
 RL Biochemistry 18:68-76(1979).  
 RN [6]  
 RP SEQUENCE OF 31-148, AND DISULFIDE BONDS.  
 RX MEDLINE=76225080; PubMed=936108;  
 RA Blomback B., Hessel B., Hogg D.;  
 RT "Disulfide bridges in NH2-terminal part of human fibrinogen.";  
 RL Thromb. Res. 8:639-658(1976).  
 RN [7]  
 RP SEQUENCE OF 1-38 FROM N.A.  
 RX MEDLINE=87146483; PubMed=3029722;  
 RA Huber P., Delmon J., Courtois G., Laurent M., Assouline Z.,  
 RA Marguerie G.;  
 RT "Characterization of the 5'-flanking region for the human fibrinogen  
 RT beta gene.";  
 RL Nucleic Acids Res. 15:1615-1625(1987).  
 RN [8]  
 RP SEQUENCE OF 31-44.  
 RA Blomback B., Blomback M., Grondahl N.J., Guthrie C., Hanton M.;  
 RT "Studies on fibrinopeptides from primates.";  
 RL Acta Chem. Scand. 19:1788-1789(1965).  
 RN [9]  
 RP REVIEW, AND DISULFIDE BONDS.  
 RX MEDLINE=83254370; PubMed=6575689;  
 RA Henschen A., Lottspeich F., Kehl M., Southan C.;  
 RT "Covalent structure of fibrinogen.";  
 RL Ann. N.Y. Acad. Sci. 408:28-43(1983).  
 RN [10]  
 RP DISULFIDE BONDS.  
 RX MEDLINE=77245999; PubMed=891553;  
 RA Gaardlund B., Hessel B., Marguerie G., Murano G., Blomback B.;  
 RT "Primary structure of human fibrinogen. Characterization of  
 RT disulfide-containing cyanogen-bromide fragments.";  
 RL Eur. J. Biochem. 77:595-610(1977).  
 RN [11]  
 RP DISULFIDE BONDS.  
 RA Doolittle R.F., Takagi T., Walt K.W.K., Bouma H. III, Cottrell B.A.,  
 RA Cassman K.G., Goldbaum D.M., Doolittle L.R., Friesner S.J.;  
 RT "The structures of fibrinogen and fibrin.";  
 RL (in) Magnusson S., Ottesen M., Foltmann B., Dano K.,  
 RL Regulatory proteolytic enzymes and their inhibitors, pp.163-172,  
 RL Pergamon Press, New York (1978).  
 RN [12]  
 RP REVIEW, EM STRUCTURE, POLYMERIZATION, AND LIGANDS.  
 RX MEDLINE=84305751; PubMed=6383194;  
 RA Doolittle R.F.;  
 RT "Fibrinogen and fibrin.";  
 RL Annu. Rev. Biochem. 53:195-229(1984).  
 RN [13]  
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 164-491.  
 RX MEDLINE=97472408; PubMed=933233;  
 RA Spraggon G., Everse S.J., Doolittle R.F.;  
 RT "Crystal structures of fragment D from human fibrinogen and its

RT crosslinked counterpart from fibrin.";  
 RL Nature 389:455-462(1997).  
 RN [14]  
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 164-491.  
 RX MEDLINE=98292395; PubMed=9628725;  
 RA Everse S.J., Spraggon G., Veerapandian L., Riley M., Doolittle R.F.;  
 RT "Crystal structure of fragment double-D from human fibrin with two  
 RT different bound ligands.";  
 RL Biochemistry 37:8637-8642(1998).  
 RN [15]  
 RP X-RAY CRYSTALLOGRAPHY.  
 RX MEDLINE=99175089; PubMed=10074346;  
 RA Everse S.J., Spraggon G., Veerapandian L., Doolittle R.F.;  
 RT "Conformational changes in fragments D and double-D from human  
 RT fibrin(ogen) upon binding the peptide ligand Gly-His-Arg-Pro-amide.";  
 RL Biochemistry 38:2941-2946(1999).  
 RN [16]  
 RP VARIANT BALTIMORE-2.  
 RX MEDLINE=89058942; PubMed=3194892;  
 RA Schmeizler C.H., Ebert R.F., Bell W.R.;  
 RT "A polymorphism at B beta 448 of fibrinogen identified during  
 RT structural studies of fibrinogen Baltimore II.";  
 RL Thromb. Res. 52:173-177(1988).  
 RN [17]  
 RP VARIANT ISE.  
 RX MEDLINE=91208409; PubMed=2018836;  
 RA Yoshida N., Wada H., Morita K., Hirata H., Matsuda M., Yamazumi K.,  
 RA Asakura S., Shirakawa S.;  
 RT "A new congenital abnormal fibrinogen Ise characterized by the  
 RT replacement of B beta glycine-15 by cysteine.";  
 RL Blood 77:1958-1963(1991).  
 RN [18]  
 RP VARIANT NAPLES.  
 RX MEDLINE=92340664; PubMed=1634610;  
 RA Koopman J., Haverkate F., Lord S.T., Grimbergen J., Mannucci P.M.;  
 RT "Molecular basis of fibrinogen Naples associated with defective  
 RT thrombin binding and thrombophilia. Homozygous substitution of B beta  
 RT 68 Ala->Thr.";  
 RL J. Clin. Invest. 90:238-244(1992).  
 RN [19]  
 RP VARIANTS IJMUIDEN AND NIJMEGEN.  
 RX MEDLINE=92228809; PubMed=1565641;  
 RA Koopman J., Haverkate F., Grimbergen J., Engesser L., Novakova I.,  
 RA Kerst A.F.J.A., Lord S.T.;  
 RT "Abnormal fibrinogens Ijmuiden (B beta Arg14->Cys) and Nijmegen (B  
 RT beta Arg44->Cys) form disulfide-linked fibrinogen-albumin  
 RT complexes.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:3478-3482(1992).  
 RN [20]  
 RP VARIANT NEW YORK-1.  
 RX MEDLINE=85157605; PubMed=3156856;  
 RA Liu C.Y., Koehn J.A., Morgan F.J.;  
 RT "Characterization of fibrinogen New York 1. A dysfunctional  
 RT fibrinogen with a deletion of B beta (9-72) corresponding exactly to  
 RT exon 2 of the gene.";  
 RL J. Biol. Chem. 260:4390-4396(1985).  
 CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT  
 CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET  
 CC AGGREGATION.  
 CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS  
 CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.  
 CC THE AMINO ENDS OF ALL CHAINS ARE CONTAINED IN THE CENTRAL NODULE.  
 CC DIVERGING FROM THIS NODULE ARE 2 THREE-CHAIN COILED COILS, WHICH  
 CC CONNECT THE CENTRAL NODULE TO THE DISTAL NODULES CONTAINING THE  
 CC DISTAL DOMAINS. EXTENDING FAR PERIPHERALLY ARE THE LONG CARBOXYL  
 CC ENDS OF THE ALPHA CHAINS.  
 CC -1- DISEASE: DEFECTS IN FGB ARE A CAUSE OF THROMBOPHILIA.  
 CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY  
 CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA  
 CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES  
 CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT. THE SOFT CLOT IS  
 CC CONVERTED INTO THE HARD CLOT BY FACTOR XIIIa WHICH CATALYZES THE  
 CC EPSILON-(GAMMA-GLUTAMYL)LYSINE CROSS-LINKING BETWEEN GAMMA CHAINS

CC (STRONGER) AND BETWEEN ALPHA CHAINS (WEAKER) OF DIFFERENT  
CC MONOMERS.  
CC -1- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.  
CC -----  
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CC -----  
DR EMBL: J00129; AAB52429.1; -  
DR EMBL: J00131; AAB98115.1; -  
DR EMBL: J00130; AAB98115.1; JOINED.  
DR EMBL: J00132; AAB98116.1; -  
DR EMBL: J00133; -; NOT\_ANNOTATED\_CDS.  
DR EMBL: X05018; CAA28674.1; -  
DR EMBL: M64983; AAB18024.2; -  
DR EMBL: M26877; AAB52445.1; -  
DR EMBL: M26876; AAB52445.1; JOINED.  
DR PIR: B43568; FGHUB.  
DR PDB: 1FZA; 03-DEC-97.  
DR PDB: 1FZB; 03-DEC-97.  
DR PDB: 1FZC; 14-OCT-98.  
DR PDB: 1FZE; 08-JUN-99.  
DR PDB: 1FZF; 08-JUN-99.  
DR PDB: 1FZG; 08-JUN-99.

Query Match 17.8%; Score 375.5; DB 1; Length 491;  
Best Local Similarity 26.6%; Pred. No. 1,8e+22;

Matches 118; Conservative 56; Mismatches 142; Indels 127; Gaps 17;

QY 25 GNCVHSTDSVYNIIVEDGSSNAKDESKSNDTYCKEDCEESCDVKKITREKHFMCRLQ 84  
D 93 GCCLHADDPLGLV-----CPGCOLLEALLQOE-----RPFR 124  
QY 85 NSI-----VSYTRSK-----KLRMMDEQASLDYLSNOVELMN----- 121  
D 125 NSVDELNNVNAVVSOTSSSFQYMYLLDLQMKRQKQVNDENVYVESSELEKHQLYTD 184  
QY 122 -----RVLLLTTEVFRKQLDPP-----HRYVSHGLDCTD 152  
D 165 ETVNSNIPINLRLVLSILENLSKIQKLESDVSAQMEYKRTCTYSCNTPYVS-GKECE 243  
QY 153 IKDTGVSATKTPSGLYIHPGESSYRFEVYCDMDYRGCGWTVIQKRIQDIIDFQRLMCDY 212  
D 244 IIRKGGET-----SEMYLLQPDSSVKKPYRYVCDMTENGSGWTVIQNRQDSVDFGRKMDY 299  
QY 213 LDGFGD-----LLGEFWLGKIKFIYIVOKNTSEMLYALAESEDDTLAYASD 260  
D 300 KQGFENVATNTDGNKYCGLPGEYWLGNDSISQLTRNGPTE--LLIEMEDWKGDKYKAHYG 357  
QY 261 NFWLEDETFEFKMLGRYSGNAGDAFRG-----LKKEDN-----QNAPEFSTSDVNDGCRP 312  
D 358 GFTYQNEANKYQISVNYKGTAGNMLMDQASQLMGENRMTHTHNGFEFTYRDNDG----- 414  
QY 313 ACLVNGQSVKSCSHLHNTGMFNECCGLANLNGIHFFSKL-----LATGIQWGTWT 364  
D 415 -WLTSDPKQCSK-EDGGWYVNRCHANPNRGYRWGQYWDMAKHGTDDGYYVMNN- 470  
QY 365 KNSPVKTIKSVSMKIRRMNPFY 387  
D 471 -KGSWYSMKRSMKIR---PFF 488

RESULT 12  
AGP2\_BOVIN STANDARD: PRT: 375 AA.

AC 077802; Q9TSKU; 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Angiotensin-2 (ANG-2) (Fragment).  
GN ANGPT2 OR ANG2.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OX NCBI\_TaxID:9913;  
RN (1)  
RP SEQUENCE FROM N.A.  
RC TISSUE-Ovary;  
RX MEDLINE:99054348; PubMed:9840613;  
RA Goede V., Schmidt T., Kimmler S., Kozian D., Augustin H.G.;  
RT "Analysis of blood vessel maturation processes during cyclic ovarian  
RT angiogenesis".  
RL Lab. Invest. 78:1385-1394(1998).  
RN (2)  
RP SEQUENCE OF 219-355 FROM N.A.  
RC TISSUE=adrenal cortex;  
RX MEDLINE:98451564; PubMed:9776732;  
RA Mandriola S.J., Pepper M.S.;  
RT "Regulation of angiotensin-2 mRNA levels in bovine microvascular  
RT endothelial cells by cytokines and hypoxia".  
RL Circ. Res. 83:852-859(1998).  
CC -1- FUNCTION: BINDS TO TIE2 RECEPTOR AND COUNTERACTS BLOOD VESSEL  
CC MATURATION/STABILITY MEDIATED BY ANGIOTENSIN-1. ITS FUNCTION MAY  
CC BE CONTEXT-DEPENDENT. IN THE ABSENCE OF ANGIOGENIC INDUCERS, SUCH  
CC AS VEGF, ANG2-MEDIATED LOOSENING OF CELL-MATRIX CONTACTS MAY  
CC INDUCE ENDOTHELIAL CELL APOPTOSIS WITH CONSEQUENT VASCULAR  
CC REGRESSION. IN CONCERT WITH VEGF, IT MAY FACILITATE ENDOTHELIAL  
CC CELL MIGRATION AND PROLIFERATION, THUS SERVING AS A PERMISSIVE  
CC ANGIOGENIC SIGNAL.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- DEVELOPMENTAL STAGE: FOUND TO BE EXPRESSED THROUGHOUT THE OVARIAN  
CC CYCLE. OVEREXPRESSION DURING LUTEOLYSIS, THIS COULD REFLECT THE  
CC REGRESSION OF CAPILLARIES THAT HAD DEVELOPED PERICYTE CONTACT IN  
CC THE MIDSTAGE CORPUS LUTEUM.  
CC -1- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.  
CC -----  
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CC -----  
DR EMBL: AF094699; AAC62490.1; -  
DR EMBL: AF032924; AAC78285.1; -  
DR HSSP: P02671; 1FZD  
DR InterPro: IPR002181; Fibrinogen\_C.  
DR Pfam: PF00147; Fibrinogen\_C; 1.  
DR SMART: SM00186; FBG; 1.  
DR PROSITE: PS00514; FIBRIN\_AG\_C\_DOMAIN; 1.  
KW Glycoprotein; Coiled coil.  
FT NON\_TER 1 1  
FT DOMAIN 10 138 COILED COIL (POTENTIAL).  
FT CARBOHYD 159 375 FIBRINOGEN C-TERMINAL.  
FT CARBOHYD 31 13 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 31 31 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 120 120 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CONFLICT 272 272 S -> L (IN REF. 2).  
SQ SEQUENCE 375 AA; 42761 MW; 6F086C4A5C80050A CRC64;

Query Match 17.8%; Score 375; DB 1; Length 375;  
Best Local Similarity 30.2%; Pred. No. 1,4e+22;

Matches 112; Conservative 57; Mismatches 136; Indels 66; Gaps 15;

QY 31 STDSVYNIIVEDGSSNAKDESKSNDTYCKE--DCESSCVKTKITREKHFHMCNRLNS 86  
D 46 STNLEKQILDTQTSLSKLDKNSFLKKVLDMEKHIVQLRSIKREKQDLQVLYSKONS 105

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RESULT 13
AGP2_MOUSE
ID AGP2_MOUSE STANDARD: PRT: 496 AA.
AC 035608;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Angiopoietin-2 precursor (ANG-2).
GN ANGPT2 OR AGPT2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RX MEDLINE=97349327; Pubmed=9204896;
RA Mazonpietre P.C., Surt C., Jones P.F., Bartunkova S., Wiegand S.J.,
RA Radziwiłłski C., Compton D.L., McClain J., Aldrich T.H.,
RA Papadopoulos N., Daly T.J., Davis S., Sato T.N., Yancopoulos G.D.;
RT "Angiopoietin-2, a natural antagonist for Tie2 that disrupts in vivo
RT angiogenesis.";
RL Science 277:55-60(1997).
CC -1- FUNCTION: BINDS TO TIE2 RECEPTOR AND COUNTERACTS BLOOD VESSEL
CC MATURATION/STABILITY MEDIATED BY ANGIOPOIETIN-1. ITS FUNCTION MAY
CC BE CONTEXT-DEPENDENT. IN THE ABSENCE OF ANGIOGENIC INDUCERS, SUCH
CC AS VEGF, ANG2-MEDIATED LOOSENING OF CELL-MATRIX CONTRACTS MAY
CC INDUCE ENDOTHELIAL CELL APOPTOSIS WITH CONSEQUENT VASCULAR
CC REGRESSION. IN CONCERT WITH VEGF, IT MAY FACILITATE ENDOTHELIAL
CC CELL MIGRATION AND PROLIFERATION, THUS SERVING AS A PERMISSIVE
CC ANGIOGENIC SIGNAL.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: EXPRESSED ONLY AT SITES OF VASCULAR
CC REMODELING.
CC -1- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AF004326; AABG3189.1; -
CC HSSP: P02671; JFZD
CC MGD: MGI:1202890; Agpt2.
CC InterPro: IPRO002181; Fibrinogen.C.

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Query Match	17.8%	Score 374.5	DB 1	Length 496
Best Local Similarity	25.5%	Pred. No. 2.2e-22		
Matches 110	Conservative 72	Mismatches 125	Indels 125	Gaps 16

QY	23	VGNHSTSTBSVNIIVEDGSMADSEKSNVTYCKEDOEESCQVKTITREKHFMCRN	82
Db	112	100NNVQNOT---AVMTIEIGTSLNQTAA-----QTRKLTVEAOVLNQTRLQL	160
QY	83	LQNSIVSTRSTPKLLRNMMDEQASLDYLSNQVNLNMRVLLTTEYF-----	131
Db	161	LQHSI-----STNKLEKQILDQ-----TSEIKLNQKNSEFLQKVLDMGKHSQQLQ	207
QY	132	-----RKQ-----LDPEPRPV-----QSHGLDCTDIKDTIGSVTK--	162
Db	208	SMKEQKDELQVLVSKROSSVIDELEKKLVATAFVNNSLQKQH-----DLMETVNSLITMM	262
QY	163	-----PPSGLIITHPESSSYPEVNMCDMDYRGCGW	192
Db	263	SSPNKSSVAIRKEBQTTFRDCAELFKSGLTSGIYTLTFPNSTELIAYCCMDGVGGGW	322
QY	193	TYIKORIGIDIFORLMDCYLDGPDLLGEPFLGLKTFIYNOKNTSPMLVALSESD	252
Db	323	TYIQHREDSVDFOPTWKYEKGFENPLGETWLGNEEYSQLGQHR--YVLKTLQKDMEG	380
QY	253	TLVASYDNFWEDETRFEKMLGRYSGNAGDAFGLKKEQNMAMPSTSDVDNDGCRP	312
Db	381	NAHSLYDHFYLAGESNRIHLTGLTGLTAAT-----SSISQPSDSTKSDNDKC--	433
QY	313	ACLVGQSVKSCSHLNKTMGMWNECGLANLNGIHH---FSGKLLATGIOWGTWTKNNS	368
Db	434	-----ICKSQMLS--GWMWFADACGPSNLNGOYYPQOKNTNKE--NGIKWYV--KGS	480
QY	369	PVKIKSVSMKIR	380
Db	481	GYSLEKATTMIMIR	492
RESULT 14			
FIBB_RAT			
ID	FIBB_RAT	STANDARD:	PRT: 479 AA.
AC	P14480:		
DT	01-JAN-1990 (Rel. 13, Created)		
DT	01-OCT-1996 (Rel. 34, Last sequence update)		
DT	01-MAR-2002 (Rel. 41, Last annotation update)		
DE	Fibrinogen beta chain precursor [Contains: Fibrinopeptide B].		
GN	FCB.		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
OX	NCBI_TaxID=10116;		
RM	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=SPRAGUE-DAWLEY; TISSUE=Liver;		
RX	MEDLINE=95143386; PubMed=7841303;		
RA	Claughton M.A., Bunce L.A., Neroni L.A., Simpson-Haidaris P.J.,		
RT	"Cloning of the complete coding sequence of rat fibrinogen B beta		

RT chain cDNA: interspecies conservation of fibrin beta 15-42 primary  
 RT structure"; Fibrinolysis 5:487-496(1994).  
 RL Blood Coagul. Fibrinolysis 5:487-496(1994).  
 RN [2]  
 RP SEQUENCE OF 1-26 FROM N.A.  
 RX MEDLINE=84194000; PubMed=6232608;  
 RA Fowles D.M., Mullis N.T., Comeau C.M., Crabtree G.R.;  
 RT "Potential basis for regulation of the coordinately expressed  
 RL fibrinogen genes: homology in the 5' flanking regions";  
 RL Proc. Natl. Acad. Sci. U.S.A. 81:2313-2316(1984).  
 RN [3]  
 RP SEQUENCE OF 19-32.  
 RA Blomback B., Blomback M., Grondahl N.J.;  
 RT "Studies on fibrinopeptides from mammals";  
 RL Acta Chem. Scand. 19:1789-1791(1965).  
 RN [4]  
 RP SEQUENCE OF 183-479 FROM N.A.  
 RX MEDLINE=69378771; PubMed=2673932;  
 RA Eastman E.M., Gillula N.B.;  
 RT "Cloning and characterization of a cDNA for the B beta chain of rat  
 RL fibrinogen: evolutionary conservation of translated and  
 RT 3'-untranslated sequences."; Gene 79:151-158(1989).  
 RL [5]  
 RP SEQUENCE OF 425-479 FROM N.A.  
 RC STRAIN=WISTAR; TISSUE=Liver;  
 RX MEDLINE=87134033; PubMed=3817019;  
 RA Sobczak J., Lotfi A.-M., Taroux P., Duguet M.;  
 RT "Molecular cloning of mRNA sequences transiently induced during rat  
 RL liver regeneration."; Exp. Cell Res. 169:47-56(1987).  
 CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT  
 CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET  
 CC AGGREGATION.  
 CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS  
 CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.  
 CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY  
 CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA  
 CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES  
 CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.  
 CC -1- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.  
 CC -----  
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 CC -----  
 DR EMBL; U05675; AAA64866.1; -;  
 DR EMBL; M27220; AAA41160.1; -;  
 DR EMBL; K01336; AAA98625.1; -;  
 DR EMBL; M35602; AAA41159.1; -;  
 DR PIR; A05299; A05299;  
 DR PIR; PE0010; PE0010;  
 DR HSBP; P02673; IPIZE.  
 DR InterPro; IPR002181; Fibrinogen\_C.  
 DR Pfam; PF00147; fibrinogen\_C; 1.  
 DR SMART; SM00186; FBG; 1.  
 DR PROSITE; PS00514; FIBRIN\_AG\_C\_DOMAIN; 1.  
 KM Blood coagulation; Plasma; Glycoprotein; Signal.  
 FT SIGNAL 1 18  
 FT CHAIN 19 479 FIBRINOGEN BETA CHAIN.  
 FT PEPTIDE 19 32 FIBRINOPEPTIDE B.  
 FT DISULFID 211 211 INTERCHAIN (WITH THE ALPHA CHAIN)  
 FT DISULFID 215 215 INTERCHAIN (WITH THE GAMMA CHAIN)  
 FT DISULFID 215 215 INTERCHAIN (WITH THE GAMMA CHAIN)  
 FT DISULFID 219 304 (BY SIMILARITY).  
 FT DISULFID 229 258 (BY SIMILARITY).  
 FT DISULFID 412 425 BY SIMILARITY.  
 FT CARBOHYD 382 382 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CONFLICT 28 30 LSI -> ILS (IN REF. 3).  
 FT CONFLICT 439 439 L -> Q (IN REF. 5).  
 FT CONFLICT 441 441 S -> T (IN REF. 5).  
 FT CONFLICT 445 445 S -> A (IN REF. 5).  
 FT CONFLICT 467 467 R -> K (IN REF. 5).  
 FT CONFLICT 475 475 V -> F (IN REF. 5).  
 SQ SEQUENCE 479 AA: 54303 MW: EC8CDB77C3B0EC0 CRC64;  
 Query Match 17.8%; Score 373.5; DB 1; Length 479;  
 Best Local Similarity 27.2%; Pred. No. 2.5e-22;  
 Matches 119; Conservative 49; Mismatches 149; Indels 121; Gaps 15;  
 QY 25 GNCVHSHDSSVNVIVEDGSAKDESKNDYVKEDESCDVTKRTREKHMKRNQ 84  
 DB 81 GCVHGDGDMGVL-----CATGCELRLQTLNHE-----RPIK 112  
 QY 85 NSIV-----SYTRSKKLLNNMDEQASLDYLSNQVNE----- 118  
 DB 113 NSIAELNSINSVETSSVTFOYLTLLKDMKKQAOYKDNENYINEXSILEDQKLYD 172  
 QY 119 -----LMNRVLTLTTEVFRKQD-----PPHPRVQSH-----GLDCTDI 153  
 DB 173 ETVNDNITPLNRVLRSILEDLSKMKQLESQISAOETECHTPCTVNCNIPYVSGKECEI 232  
 QY 154 KDTIGSVTKPTSGLYIHPESSYPFEVCMQDYGCGMTVIQRTDGIIDFQRLMCDYL 213  
 DB 233 IRKGSET-----SEWLIOPDTRSKRYVCDMKTEENGMTVIQNDQSDVDFGRKMDPK 288  
 QY 214 DGFGD-----LLGFEVLGLKRTFYIVNKNISFPLVALBESDITLAVASYDN 261  
 DB 289 KFGNIAINEDTKKYGCGIPGEVWLGNDKISQITRIGPE--LLEMEWKGDKYKAHGG 346  
 QY 262 FWLEDETRFFKMLHGRYSNGADAF---RLKKEDN---QNAPEFSTDVDNDGCRPA 313  
 DB 347 FTVQTEANKKYQVSVKRYGTAGNMLBEGASQLVGNRTMTIHNGFFETVYRDNDG---- 402  
 QY 314 CLVNGSVKSCSHLHNTKGMFMFNECGLANLNGIHHSKGL-----LATGIQGTWTK 365  
 DB 403 -WVTIDPRKQCSK-EDGGWWMYNRCHAMPNGRYWGLYSWMSKHTGDDGVVMMN- 458  
 QY 366 NNSPVKIKSVSMKIRMY 383  
 DB 459 KGSWYSMRMSKKTIPVF 476  
 RESULT 15  
 FTBB\_CHICK  
 ID FTBB\_CHICK STANDARD; PRT: 463 AA.  
 AC 002020;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Fibrinogen beta chain precursor [Contains: Fibrinopeptide B]  
 DE (Fragment).  
 GN FGB.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 CC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-13 AND 18-39.  
 RX MEDLINE=91182745; PubMed=2009266;  
 RA Weissbach L., Odoux C., Procyk R., Grieninger G.;  
 RT "The beta chain of chicken fibrinogen contains an atypical thrombin  
 RL cleavage site"; Biochemistry 30:3290-3294(1991).  
 CC Biochemistry 30:3290-3294(1991).  
 CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT  
 CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET  
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